



wwPDB EM Validation Summary Report ⓘ

Nov 30, 2022 – 01:13 pm GMT

PDB ID : 7ZME
EMDB ID : EMD-14796
Title : CryoEM structure of mitochondrial complex I from *Chaetomium thermophilum* (state 2) - membrane arm
Authors : Laube, E.; Kuehlbrandt, W.
Deposited on : 2022-04-19
Resolution : 2.83 Å (reported)
Based on initial models : 6RFQ, 6RFR

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

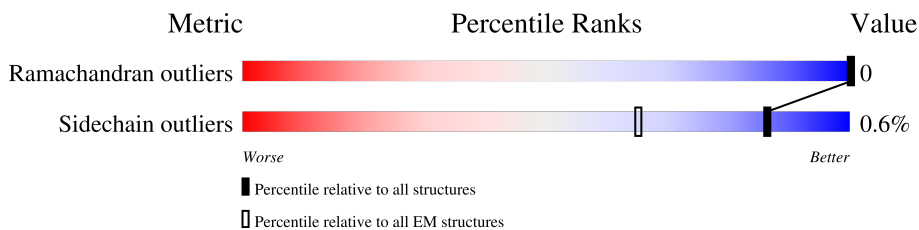
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.83 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



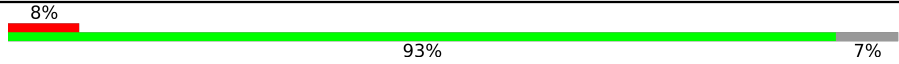
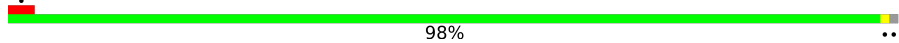

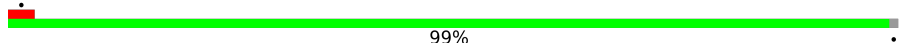






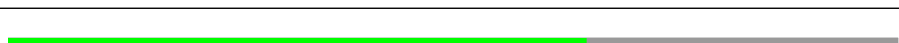

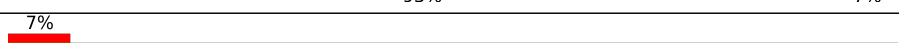
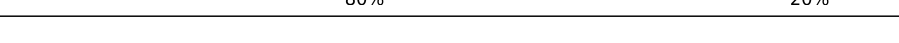
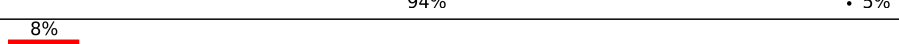
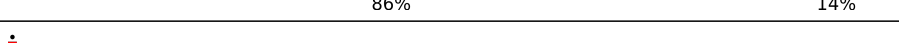
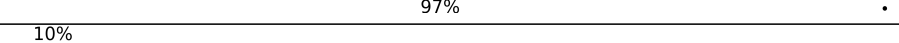
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	378	87% 12%
2	2	571	96% ..
3	3	146	77% 22%
4	4	542	91% 9%
5	5	679	98% ..
6	6	224	83% 15%
7	8	86	90% 10% 12%
8	9	785	87% 13%
9	D	86	98% ..

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Mol	Chain	Length	Quality of chain
10	J	199	
11	L	89	
12	Q	141	
13	R	99	
14	S	143	
15	U	186	
16	W	121	
17	X	191	
18	a	815	
19	b	94	
20	c	93	
21	d	105	
22	e	46	
23	g	82	
24	i	93	
25	j	75	
26	n	184	

2 Entry composition i

There are 32 unique types of molecules in this entry. The entry contains 36964 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	1	334	2573	1728	388	446	11	0	0

- Molecule 2 is a protein called NADH dehydrogenase subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	2	558	4456	2993	672	780	11	0	0

- Molecule 3 is a protein called NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	114	907	619	132	153	3	0	0

- Molecule 4 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	4	494	3904	2650	572	670	12	0	0

- Molecule 5 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	5	670	5272	3551	792	904	25	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	445	ARG	-	insertion	UNP G1DJA3
5	446	LEU	-	insertion	UNP G1DJA3
5	447	ALA	-	insertion	UNP G1DJA3

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Chain	Residue	Modelled	Actual	Comment	Reference
5	448	ILE	-	insertion	UNP G1DJA3
5	449	ASP	-	insertion	UNP G1DJA3
5	450	ASN	-	insertion	UNP G1DJA3
5	451	PHE	-	insertion	UNP G1DJA3
5	452	PHE	-	insertion	UNP G1DJA3
5	453	SER	-	insertion	UNP G1DJA3
5	454	ALA	-	insertion	UNP G1DJA3
5	455	GLN	-	insertion	UNP G1DJA3
5	456	ALA	-	insertion	UNP G1DJA3
5	457	ILE	-	insertion	UNP G1DJA3
5	458	LYS	-	insertion	UNP G1DJA3

- Molecule 6 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	6	190	1454	981	219	248	6	0	0

- Molecule 7 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	8	77	658	408	126	118	6	0	0

- Molecule 8 is a protein called Subunit NDUFS5 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	9	103	807	500	147	154	6	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
9	100	VAL	-	insertion	UNP G0SG48

- Molecule 9 is a protein called Subunit NDUFA1 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	85	Total	C	N	O	S	0	0
			678	432	127	115	4		

- Molecule 10 is a protein called NADH-ubiquinone oxidoreductase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	186	Total	C	N	O	S	0	0
			1375	872	259	242	2		

- Molecule 11 is a protein called NADH-ubiquinone oxidoreductase chain 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	88	Total	C	N	O	S	0	0
			671	450	103	115	3		

- Molecule 12 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Q	85	Total	C	N	O	S	0	0
			663	418	109	135	1		

- Molecule 13 is a protein called Complex I-B22.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	R	98	Total	C	N	O	S	0	0
			807	520	149	137	1		

- Molecule 14 is a protein called Complex I-ESSS.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	S	74	Total	C	N	O	0	0
			610	401	98	111		

- Molecule 15 is a protein called NADH-ubiquinone oxidoreductase.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	U	169	Total	C	N	O	S	0	0
			1365	860	254	242	9		

- Molecule 16 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	W	99	812	519	154	137	2	0	0

- Molecule 17 is a protein called NADH-ubiquinone oxidoreductase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	X	187	1480	941	268	263	8	0	0

- Molecule 18 is a protein called NADH dehydrogenase (Ubiquinone)-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	a	143	1167	750	195	217	5	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	166	VAL	ALA	conflict	UNP G0RXU4
a	168	ALA	MET	conflict	UNP G0RXU4
a	?	-	GLU	deletion	UNP G0RXU4
a	?	-	GLY	deletion	UNP G0RXU4
a	?	-	ASP	deletion	UNP G0RXU4
a	?	-	PRO	deletion	UNP G0RXU4
a	?	-	ASP	deletion	UNP G0RXU4
a	?	-	PRO	deletion	UNP G0RXU4

- Molecule 19 is a protein called Subunit NDUFC2 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	b	81	683	445	125	110	3	0	0

- Molecule 20 is a protein called Subunit NDUF3 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	c	60	490	320	86	82	2	0	0

- Molecule 21 is a protein called Subunit NDUF10 of NADH-ubiquinone oxidoreductase

(Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	d	98	817	520	144	149	4	0	0

- Molecule 22 is a protein called Subunit NDUFB2 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	e	37	309	211	54	43	1	0	0

- Molecule 23 is a protein called Subunit NDUF3 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	g	78	610	399	105	105	1	0	0

- Molecule 24 is a protein called Subunit NDUF6 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	i	80	677	447	117	111	2	0	0

- Molecule 25 is a protein called Subunit NDUF4 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	j	73	603	391	108	101	3	0	0

- Molecule 26 is a protein called Subunit NDUF5 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	n	135	1061	680	186	194	1	0	0

There are 52 discrepancies between the modelled and reference sequences:

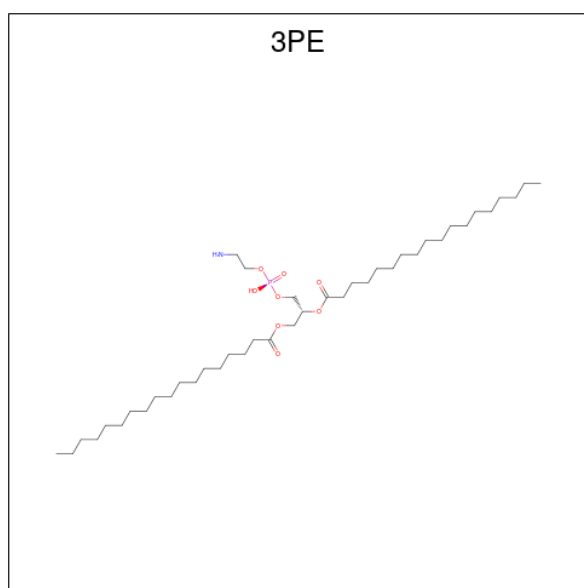
Chain	Residue	Modelled	Actual	Comment	Reference
n	1	MET	-	initiating methionine	UNP G0S086
n	2	LEU	-	insertion	UNP G0S086
n	3	ALA	-	insertion	UNP G0S086
n	4	LEU	-	insertion	UNP G0S086
n	5	ARG	-	insertion	UNP G0S086
n	6	GLN	-	insertion	UNP G0S086
n	7	ARG	-	insertion	UNP G0S086
n	8	ALA	-	insertion	UNP G0S086
n	9	ALA	-	insertion	UNP G0S086
n	10	LEU	-	insertion	UNP G0S086
n	11	LEU	-	insertion	UNP G0S086
n	12	ALA	-	insertion	UNP G0S086
n	13	ARG	-	insertion	UNP G0S086
n	14	ARG	-	insertion	UNP G0S086
n	15	VAL	-	insertion	UNP G0S086
n	16	ARG	-	insertion	UNP G0S086
n	17	PRO	-	insertion	UNP G0S086
n	18	THR	-	insertion	UNP G0S086
n	19	VAL	-	insertion	UNP G0S086
n	20	VAL	-	insertion	UNP G0S086
n	21	VAL	-	insertion	UNP G0S086
n	22	PRO	-	insertion	UNP G0S086
n	23	ARG	-	insertion	UNP G0S086
n	24	ASN	-	amidation	UNP G0S086
n	25	ALA	-	insertion	UNP G0S086
n	26	ARG	-	insertion	UNP G0S086
n	27	THR	-	insertion	UNP G0S086
n	28	TYR	-	insertion	UNP G0S086
n	29	ALA	-	insertion	UNP G0S086
n	30	SER	-	insertion	UNP G0S086
n	31	SER	-	insertion	UNP G0S086
n	32	HIS	-	insertion	UNP G0S086
n	33	ASP	-	insertion	UNP G0S086
n	34	HIS	-	insertion	UNP G0S086
n	35	ASP	-	insertion	UNP G0S086
n	36	HIS	-	insertion	UNP G0S086
n	37	HIS	-	insertion	UNP G0S086
n	38	ASP	-	insertion	UNP G0S086
n	39	HIS	-	insertion	UNP G0S086
n	40	HIS	-	insertion	UNP G0S086
n	41	HIS	-	insertion	UNP G0S086
n	42	ASP	-	insertion	UNP G0S086
n	43	HIS	-	insertion	UNP G0S086

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Chain	Residue	Modelled	Actual	Comment	Reference
n	44	GLY	-	insertion	UNP G0S086
n	45	HIS	-	insertion	UNP G0S086
n	46	ASN	-	insertion	UNP G0S086
n	47	VAL	-	insertion	UNP G0S086
n	48	GLU	-	insertion	UNP G0S086
n	49	GLU	-	insertion	UNP G0S086
n	50	PRO	-	insertion	UNP G0S086
n	51	LEU	-	insertion	UNP G0S086
n	52	GLY	-	insertion	UNP G0S086

- Molecule 27 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (three-letter code: 3PE) (formula: C₄₁H₈₂NO₈P).



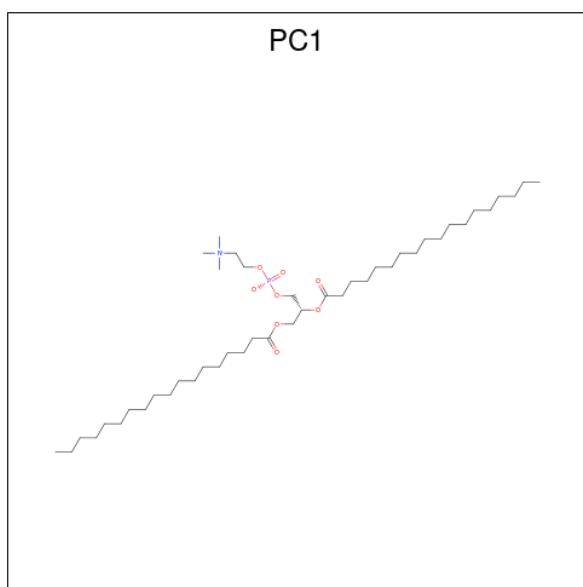
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
27	1	1	Total	C	N	O	P	0
			68	49	2	15	2	
27	1	1	Total	C	N	O	P	0
			68	49	2	15	2	
27	4	1	Total	C	N	O	P	0
			95	65	3	24	3	
27	4	1	Total	C	N	O	P	0
			95	65	3	24	3	
27	4	1	Total	C	N	O	P	0
			95	65	3	24	3	
27	5	1	Total	C	N	O	P	0
			142	102	4	32	4	

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
27	5	1	Total 142	C 102	N 4	O 32	P 4	0
27	5	1	Total 142	C 102	N 4	O 32	P 4	0
27	5	1	Total 142	C 102	N 4	O 32	P 4	0
27	8	1	Total 36	C 26	N 1	O 8	P 1	0
27	J	1	Total 30	C 20	N 1	O 8	P 1	0
27	W	1	Total 34	C 24	N 1	O 8	P 1	0
27	g	1	Total 75	C 55	N 2	O 16	P 2	0
27	g	1	Total 75	C 55	N 2	O 16	P 2	0
27	n	1	Total 78	C 58	N 2	O 16	P 2	0
27	n	1	Total 78	C 58	N 2	O 16	P 2	0

- Molecule 28 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PC1) (formula: $C_{44}H_{88}NO_8P$).



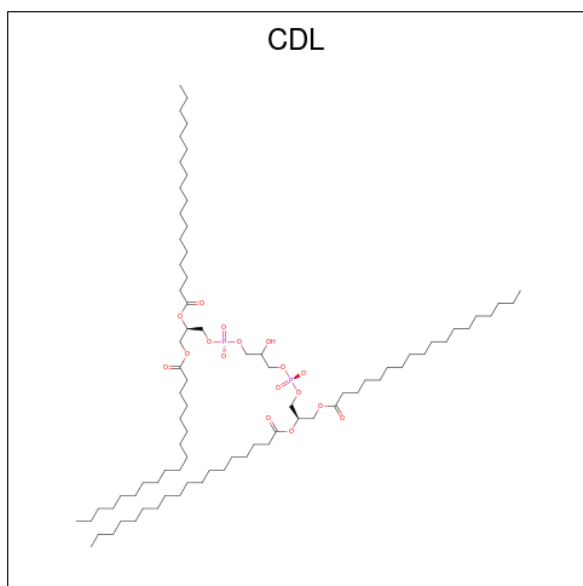
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
28	1	1	Total 30	C 20	N 1	O 8	P 1	0

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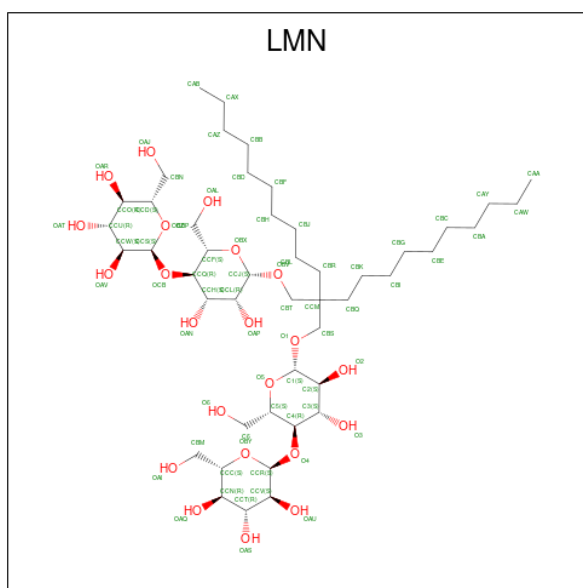
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
28	2	1	Total 31	C 21	N 1	O 8	P 1	0
28	3	1	Total 36	C 26	N 1	O 8	P 1	0
28	4	1	Total 45	C 35	N 1	O 8	P 1	0
28	5	1	Total 86	C 66	N 2	O 16	P 2	0
28	5	1	Total 86	C 66	N 2	O 16	P 2	0
28	n	1	Total 51	C 41	N 1	O 8	P 1	0

- Molecule 29 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



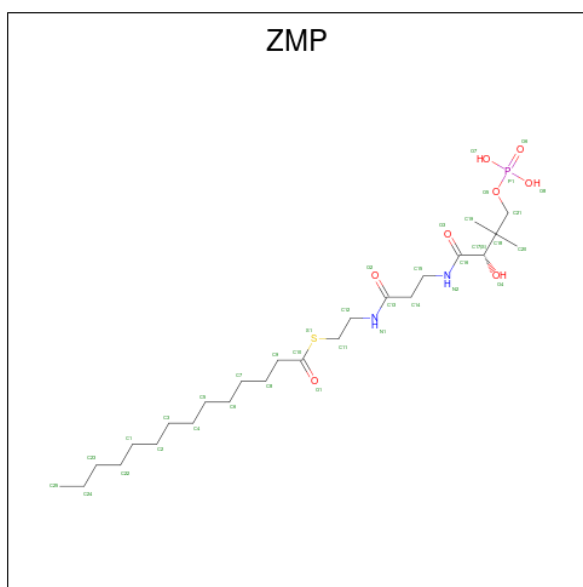
Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
29	2	1	Total 84	C 65	O 17	P 2	0
29	4	1	Total 86	C 67	O 17	P 2	0
29	D	1	Total 59	C 40	O 17	P 2	0
29	X	1	Total 79	C 60	O 17	P 2	0
29	g	1	Total 56	C 37	O 17	P 2	0

- Molecule 30 is Lauryl Maltose Neopentyl Glycol (three-letter code: LMN) (formula: $C_{47}H_{88}O_{22}$).



Mol	Chain	Residues	Atoms	AltConf
30	2	1	Total C O 58 41 17	0
30	4	1	Total C O 58 41 17	0
30	J	1	Total C O 69 47 22	0

- Molecule 31 is S-[2-({N-[(2S)-2-hydroxy-3,3-dimethyl-4-(phosphonoxy)butanoyl]-beta-alanyl}amino)ethyl] tetradecanethioate (three-letter code: ZMP) (formula: $C_{25}H_{49}N_2O_8PS$).



Mol	Chain	Residues	Atoms					AltConf	
			Total	C	N	O	P		S
31	Q	1	36	25	2	7	1	1	0

- Molecule 32 is water.

Mol	Chain	Residues	Atoms		AltConf
32	1	62	Total 62	O 62	0
32	2	141	Total 141	O 141	0
32	3	24	Total 24	O 24	0
32	4	84	Total 84	O 84	0
32	5	49	Total 49	O 49	0
32	6	35	Total 35	O 35	0
32	9	19	Total 19	O 19	0
32	D	27	Total 27	O 27	0
32	J	1	Total 1	O 1	0
32	L	11	Total 11	O 11	0
32	R	4	Total 4	O 4	0
32	S	1	Total 1	O 1	0
32	U	36	Total 36	O 36	0
32	W	29	Total 29	O 29	0
32	X	45	Total 45	O 45	0
32	a	11	Total 11	O 11	0
32	b	4	Total 4	O 4	0
32	d	9	Total 9	O 9	0
32	g	10	Total 10	O 10	0

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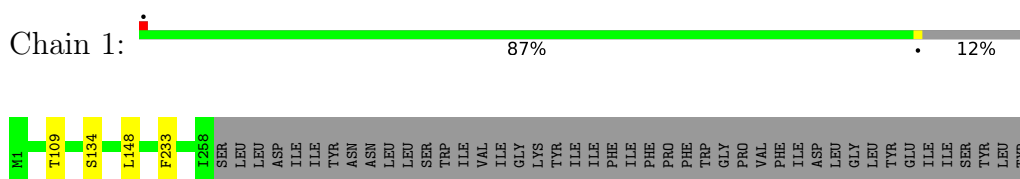
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Mol	Chain	Residues	Atoms		AltConf
32	i	4	Total 4	O 4	0
32	j	4	Total 4	O 4	0
32	n	23	Total 23	O 23	0

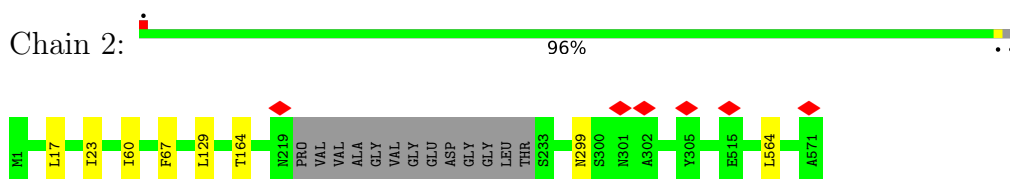
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

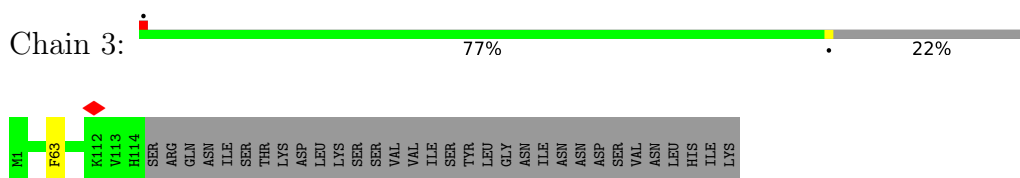
- Molecule 1: NADH-ubiquinone oxidoreductase chain 1



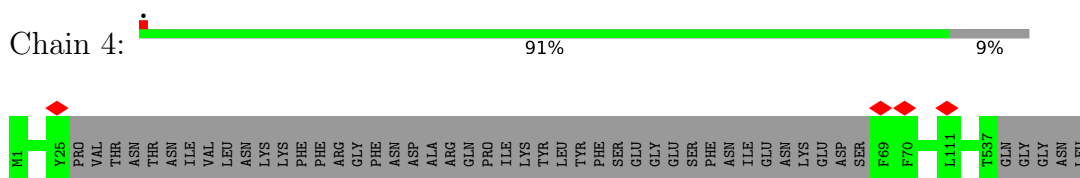
- Molecule 2: NADH dehydrogenase subunit 2



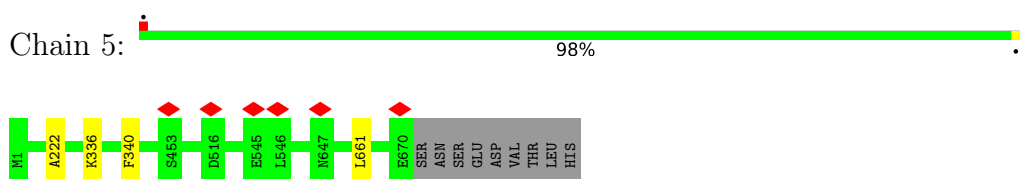
- Molecule 3: NADH-ubiquinone oxidoreductase chain 3



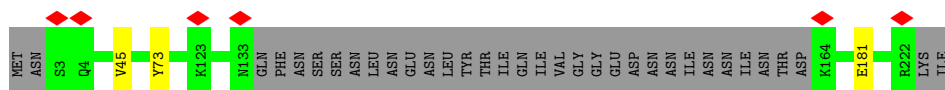
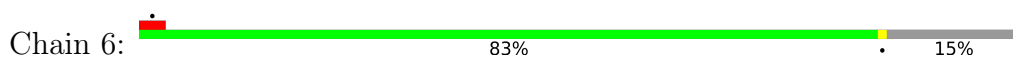
- Molecule 4: NADH-ubiquinone oxidoreductase chain 4



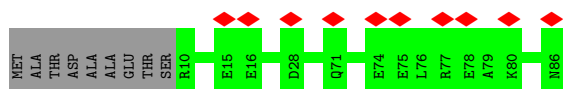
- Molecule 5: NADH-ubiquinone oxidoreductase chain 5



- Molecule 6: NADH-ubiquinone oxidoreductase chain 6



- Molecule 7: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7



- Molecule 8: Subunit NDUF5 of NADH-ubiquinone oxidoreductase (Complex I)

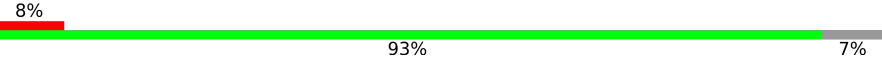


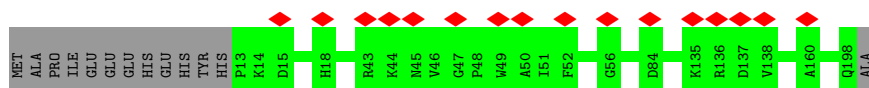
- Molecule 9: Subunit NDUFA1 of NADH-ubiquinone oxidoreductase (Complex I)

Chain D:  98%



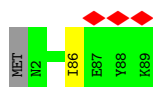
- Molecule 10: NADH-ubiquinone oxidoreductase-like protein

Chain J:  8% 93% 7%



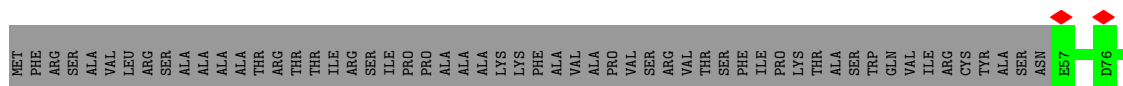
- Molecule 11: NADH-ubiquinone oxidoreductase chain 4L

Chain L:  98%



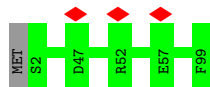
- Molecule 12: Acyl carrier protein

Chain Q:  60% 40%



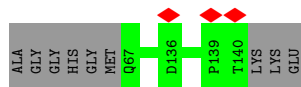
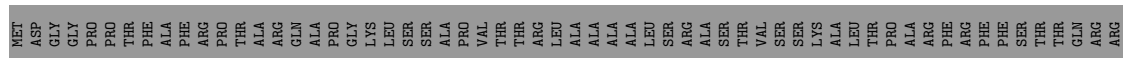
- Molecule 13: Complex I-B22

Chain R:  99%



- Molecule 14: Complex I-ESSS

Chain S:  52% 48%

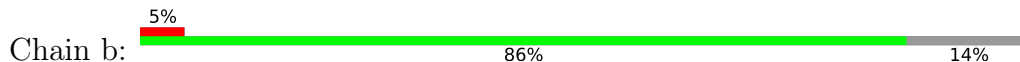


- Molecule 15: NADH-ubiquinone oxidoreductase

THR ASP VAL GLN VAL GLU PRO PRO ALA ALA THR SER SER ASN ALA ALA ASN SER SER VAL ILE ASN THR SER GLY THR SER THR THR THR VAL HIS ALA ASN VAL PRO THR SER SER LYS ARG PRO ARG ASN PHE THR PRO ALA ALA ARG VAL ILE ASP GLU GLU ASP GLU

PRO ARG THR SER PRO GLN VAL GLN VAL GLY PHE ALA GLU THR SER VAL GLU SER ILE GLN

- Molecule 19: Subunit NDUFC2 of NADH-ubiquinone oxidoreductase (Complex I)



M1 R30 Q79 A80 E81 ALA ALA ALA THR ALA PRO SER PRO SER ALA GLN GLU ALA

- Molecule 20: Subunit NDUF3 of NADH-ubiquinone oxidoreductase (Complex I)



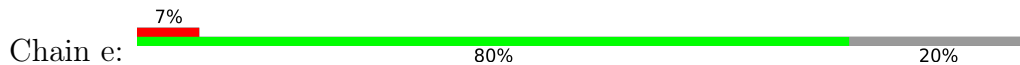
MET GLN PRO THR ARG ILE LEU ARG ASN GLN GLY LYS F14 Y73 PHE GLU HIS PHE LEU LYS ASP HIS HIS GLY HIS HIS GLY LYS GLU LYS HIS HIS

- Molecule 21: Subunit NDUF10 of NADH-ubiquinone oxidoreductase (Complex I)



MET P2 E7 S99 LYS GLU ASN GLN GLN

- Molecule 22: Subunit NDUF2 of NADH-ubiquinone oxidoreductase (Complex I)



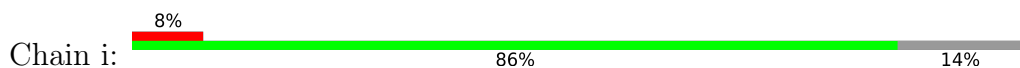
MET ALA GLY GLY GLN HIS VAL S9 K32 L39 K42 W45 ASP

- Molecule 23: Subunit NDUF3 of NADH-ubiquinone oxidoreductase (Complex I)



MET SER ALA T4 R17 D61 ASN

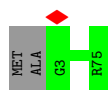
- Molecule 24: Subunit NDUF6 of NADH-ubiquinone oxidoreductase (Complex I)




MET GLY GLY GLY P5 D76 Y77 E78 R79 A80 Q81 K82 E83 K84 GLN GLN ASN ASN THR THR ALA SER SER

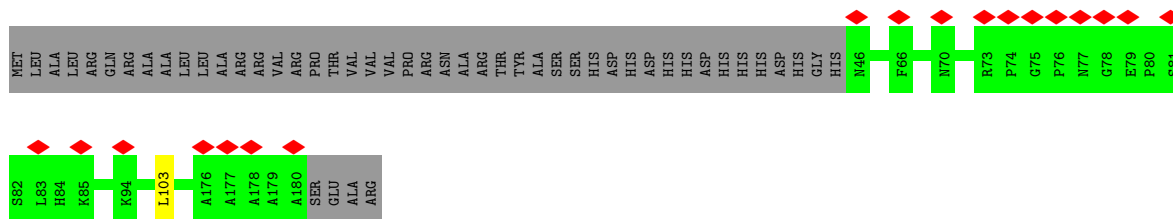
- Molecule 25: Subunit NDUFB4 of NADH-ubiquinone oxidoreductase (Complex I)

Chain j:  97%



- Molecule 26: Subunit NDUFB5 of NADH-ubiquinone oxidoreductase (Complex I)

Chain n:  10% 73% 27%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21989	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.226	Depositor
Minimum map value	-1.186	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.133	Depositor
Recommended contour level	0.12	Depositor
Map size (\AA)	143.964, 218.457, 227.664	wwPDB
Map dimensions	272, 261, 172	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.837, 0.837, 0.837	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 3PE, ZMP, CDL, PC1, LMN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.46	0/2633	0.62	0/3593
2	2	0.46	0/4562	0.61	1/6205 (0.0%)
3	3	0.43	0/934	0.56	0/1269
4	4	0.40	0/4002	0.54	0/5454
5	5	0.38	1/5414 (0.0%)	0.55	2/7371 (0.0%)
6	6	0.53	2/1481 (0.1%)	0.65	0/2020
7	8	0.27	0/671	0.43	0/896
8	9	0.40	0/824	0.56	0/1112
9	D	0.52	0/674	0.74	0/911
10	J	0.33	0/1400	0.48	0/1892
11	L	0.45	0/677	0.58	0/917
12	Q	0.28	0/673	0.47	0/913
13	R	0.33	0/832	0.48	0/1133
14	S	0.34	0/635	0.49	0/869
15	U	0.48	0/1403	0.69	0/1904
16	W	0.47	0/830	0.70	0/1120
17	X	0.50	0/1519	0.66	0/2053
18	a	0.32	0/1204	0.47	0/1632
19	b	0.29	0/701	0.40	0/939
20	c	0.28	0/509	0.45	0/691
21	d	0.35	0/835	0.47	0/1123
22	e	0.36	0/324	0.45	0/440
23	g	0.42	0/631	0.60	0/868
24	i	0.34	0/706	0.49	0/960
25	j	0.32	0/617	0.44	0/830
26	n	0.44	0/1092	0.58	0/1481
All	All	0.41	3/35783 (0.0%)	0.57	3/48596 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	6	45	VAL	C-N	-5.52	1.21	1.34
6	6	181	GLU	C-N	5.52	1.46	1.34
5	5	222	ALA	C-N	-5.05	1.22	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	5	661	LEU	CB-CG-CD2	-7.43	98.37	111.00
5	5	661	LEU	CA-CB-CG	6.20	129.56	115.30
2	2	67	PHE	CB-CA-C	5.21	120.83	110.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	330/378 (87%)	317 (96%)	13 (4%)	0	100	100
2	2	554/571 (97%)	545 (98%)	9 (2%)	0	100	100
3	3	112/146 (77%)	108 (96%)	4 (4%)	0	100	100
4	4	490/542 (90%)	479 (98%)	11 (2%)	0	100	100
5	5	668/679 (98%)	638 (96%)	30 (4%)	0	100	100
6	6	186/224 (83%)	178 (96%)	8 (4%)	0	100	100
7	8	75/86 (87%)	71 (95%)	4 (5%)	0	100	100
8	9	101/785 (13%)	100 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	D	79/86 (92%)	78 (99%)	1 (1%)	0	100	100
10	J	184/199 (92%)	179 (97%)	5 (3%)	0	100	100
11	L	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
12	Q	83/141 (59%)	83 (100%)	0	0	100	100
13	R	96/99 (97%)	93 (97%)	3 (3%)	0	100	100
14	S	72/143 (50%)	68 (94%)	4 (6%)	0	100	100
15	U	167/186 (90%)	162 (97%)	5 (3%)	0	100	100
16	W	97/121 (80%)	97 (100%)	0	0	100	100
17	X	185/191 (97%)	182 (98%)	3 (2%)	0	100	100
18	a	141/815 (17%)	136 (96%)	5 (4%)	0	100	100
19	b	79/94 (84%)	78 (99%)	1 (1%)	0	100	100
20	c	58/93 (62%)	50 (86%)	8 (14%)	0	100	100
21	d	96/105 (91%)	92 (96%)	4 (4%)	0	100	100
22	e	35/46 (76%)	35 (100%)	0	0	100	100
23	g	76/82 (93%)	74 (97%)	2 (3%)	0	100	100
24	i	78/93 (84%)	75 (96%)	3 (4%)	0	100	100
25	j	71/75 (95%)	68 (96%)	3 (4%)	0	100	100
26	n	133/184 (72%)	129 (97%)	4 (3%)	0	100	100
All	All	4332/6253 (69%)	4198 (97%)	134 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	284/326 (87%)	280 (99%)	4 (1%)	67	83
2	2	509/518 (98%)	502 (99%)	7 (1%)	67	83
3	3	97/128 (76%)	96 (99%)	1 (1%)	76	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	4	431/477 (90%)	431 (100%)	0	100	100
5	5	579/596 (97%)	577 (100%)	2 (0%)	92	96
6	6	162/203 (80%)	161 (99%)	1 (1%)	86	93
7	8	69/75 (92%)	69 (100%)	0	100	100
8	9	84/687 (12%)	84 (100%)	0	100	100
9	D	68/69 (99%)	67 (98%)	1 (2%)	65	82
10	J	126/146 (86%)	126 (100%)	0	100	100
11	L	73/76 (96%)	72 (99%)	1 (1%)	67	83
12	Q	72/119 (60%)	72 (100%)	0	100	100
13	R	87/89 (98%)	87 (100%)	0	100	100
14	S	59/111 (53%)	59 (100%)	0	100	100
15	U	149/167 (89%)	147 (99%)	2 (1%)	69	84
16	W	82/102 (80%)	82 (100%)	0	100	100
17	X	145/152 (95%)	143 (99%)	2 (1%)	67	83
18	a	123/697 (18%)	123 (100%)	0	100	100
19	b	67/74 (90%)	67 (100%)	0	100	100
20	c	47/80 (59%)	47 (100%)	0	100	100
21	d	87/94 (93%)	87 (100%)	0	100	100
22	e	29/35 (83%)	29 (100%)	0	100	100
23	g	65/69 (94%)	64 (98%)	1 (2%)	65	82
24	i	68/78 (87%)	68 (100%)	0	100	100
25	j	63/64 (98%)	63 (100%)	0	100	100
26	n	106/150 (71%)	105 (99%)	1 (1%)	78	89
All	All	3731/5382 (69%)	3708 (99%)	23 (1%)	86	93

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	6	73	TYR
15	U	15	ASP
11	L	86	ILE
15	U	23	ILE
2	2	60	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
13	R	24	HIS
15	U	56	GLN
14	S	117	GLN
15	U	149	GLN
5	5	171	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

32 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
27	3PE	4	603	-	32,32,50	1.05	4 (12%)	35,37,55	1.17	2 (5%)
27	3PE	1	402	-	26,26,50	0.34	0	28,30,55	0.54	0
28	PC1	4	605	-	44,44,53	1.02	4 (9%)	50,52,61	1.06	2 (4%)
27	3PE	5	702	-	39,39,50	0.30	0	42,44,55	0.36	0
27	3PE	n	201	-	38,38,50	0.99	4 (10%)	41,43,55	1.14	2 (4%)
27	3PE	5	706	-	27,27,50	1.07	3 (11%)	30,32,55	1.16	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
28	PC1	2	603	-	30,30,53	0.34	0	36,38,61	0.37	0
29	CDL	X	201	-	78,78,99	0.31	0	84,90,111	0.40	0
30	LMN	J	202	-	72,72,72	0.16	0	96,98,98	0.29	0
27	3PE	5	703	-	31,31,50	1.08	4 (12%)	34,36,55	1.16	2 (5%)
27	3PE	5	704	-	41,41,50	0.95	4 (9%)	44,46,55	1.09	2 (4%)
28	PC1	3	201	-	35,35,53	0.34	0	41,43,61	0.39	0
27	3PE	W	201	-	33,33,50	0.31	0	34,37,55	0.40	0
29	CDL	g	101	-	55,55,99	0.35	0	61,67,111	0.55	0
30	LMN	2	602	-	60,60,72	0.20	0	78,80,98	0.54	1 (1%)
28	PC1	n	202	-	50,50,53	0.96	4 (8%)	56,58,61	1.08	2 (3%)
29	CDL	D	101	-	58,58,99	0.34	0	64,70,111	0.44	0
28	PC1	5	705	-	40,40,53	1.08	3 (7%)	46,48,61	1.14	3 (6%)
27	3PE	J	201	-	29,29,50	1.12	4 (13%)	32,34,55	1.18	2 (6%)
29	CDL	4	601	-	85,85,99	0.28	0	91,97,111	0.35	0
30	LMN	4	604	-	60,60,72	0.19	0	78,80,98	0.32	0
28	PC1	1	403	-	29,29,53	1.26	4 (13%)	35,37,61	1.25	2 (5%)
28	PC1	5	701	-	44,44,53	0.44	0	50,52,61	0.46	0
27	3PE	g	102	-	35,35,50	0.33	0	38,40,55	0.47	0
27	3PE	g	103	-	38,38,50	0.35	0	41,43,55	0.38	0
27	3PE	4	602	-	33,33,50	1.04	4 (12%)	36,38,55	1.13	2 (5%)
27	3PE	1	401	-	40,40,50	0.39	0	43,45,55	0.43	0
29	CDL	2	601	-	83,83,99	0.31	0	89,95,111	0.36	0
31	ZMP	Q	201	12	29,35,36	0.19	0	34,42,45	0.45	0
27	3PE	8	101	-	35,35,50	1.02	4 (11%)	38,40,55	1.13	2 (5%)
27	3PE	n	203	-	38,38,50	0.98	4 (10%)	41,43,55	1.12	2 (4%)
27	3PE	4	606	-	27,27,50	1.15	4 (14%)	30,32,55	1.18	2 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
27	3PE	4	603	-	-	22/36/36/54	-
27	3PE	1	402	-	-	8/29/29/54	-
28	PC1	4	605	-	-	30/48/48/57	-
27	3PE	5	702	-	-	13/43/43/54	-
27	3PE	n	201	-	-	17/42/42/54	-
27	3PE	5	706	-	-	9/30/30/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	PC1	2	603	-	-	8/34/34/57	-
29	CDL	X	201	-	-	25/89/89/110	-
30	LMN	J	202	-	-	11/50/130/130	0/4/4/4
27	3PE	5	703	-	-	11/35/35/54	-
27	3PE	5	704	-	-	16/45/45/54	-
28	PC1	3	201	-	-	11/39/39/57	-
27	3PE	W	201	-	-	12/36/36/54	-
29	CDL	g	101	-	-	16/66/66/110	-
30	LMN	2	602	-	-	18/44/104/130	0/3/3/4
28	PC1	n	202	-	-	20/54/54/57	-
29	CDL	D	101	-	-	28/69/69/110	-
28	PC1	5	705	-	-	22/44/44/57	-
27	3PE	J	201	-	-	14/33/33/54	-
29	CDL	4	601	-	-	26/96/96/110	-
30	LMN	4	604	-	-	15/44/104/130	0/3/3/4
28	PC1	1	403	-	-	17/32/32/57	-
28	PC1	5	701	-	-	20/48/48/57	-
27	3PE	g	102	-	-	17/39/39/54	-
27	3PE	g	103	-	-	15/42/42/54	-
27	3PE	4	602	-	-	12/37/37/54	-
27	3PE	1	401	-	-	9/44/44/54	-
29	CDL	2	601	-	-	24/94/94/110	-
31	ZMP	Q	201	12	-	10/40/42/43	-
27	3PE	8	101	-	-	18/39/39/54	-
27	3PE	n	203	-	-	19/42/42/54	-
27	3PE	4	606	-	-	8/31/31/54	-

The worst 5 of 54 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	5	705	PC1	O21-C2	-2.69	1.39	1.46
27	n	201	3PE	O21-C2	-2.55	1.40	1.46
27	4	606	3PE	O21-C2	-2.51	1.40	1.46
27	5	704	3PE	O21-C2	-2.51	1.40	1.46
27	4	602	3PE	O21-C2	-2.50	1.40	1.46

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	403	PC1	O21-C21-C22	4.87	120.05	111.09
27	n	201	3PE	O21-C21-C22	4.15	120.44	111.50
28	4	605	PC1	O21-C21-C22	4.13	120.41	111.50
28	n	202	PC1	O21-C21-C22	4.12	120.39	111.50
27	5	706	3PE	O21-C21-C22	4.12	120.37	111.50

There are no chirality outliers.

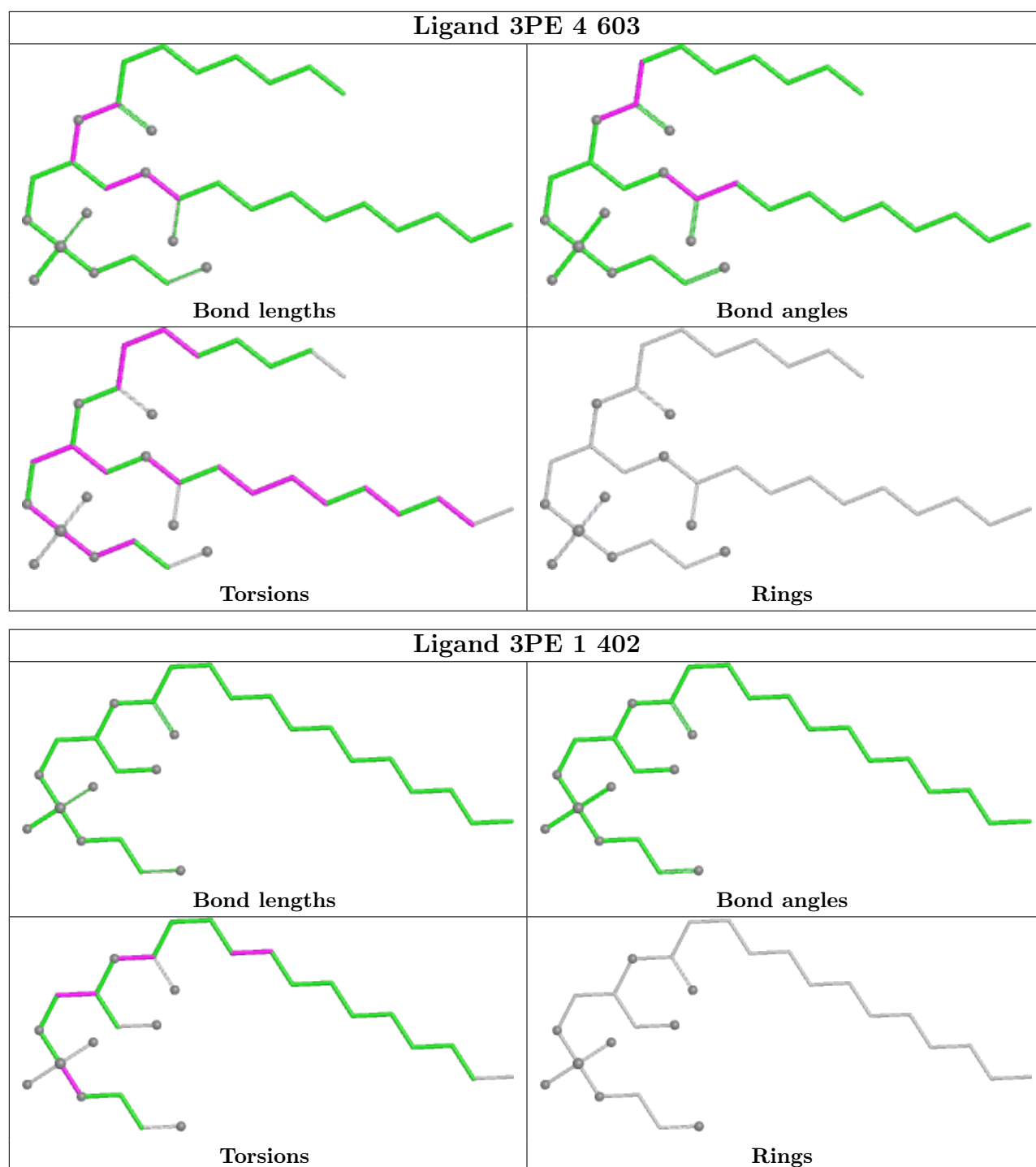
5 of 521 torsion outliers are listed below:

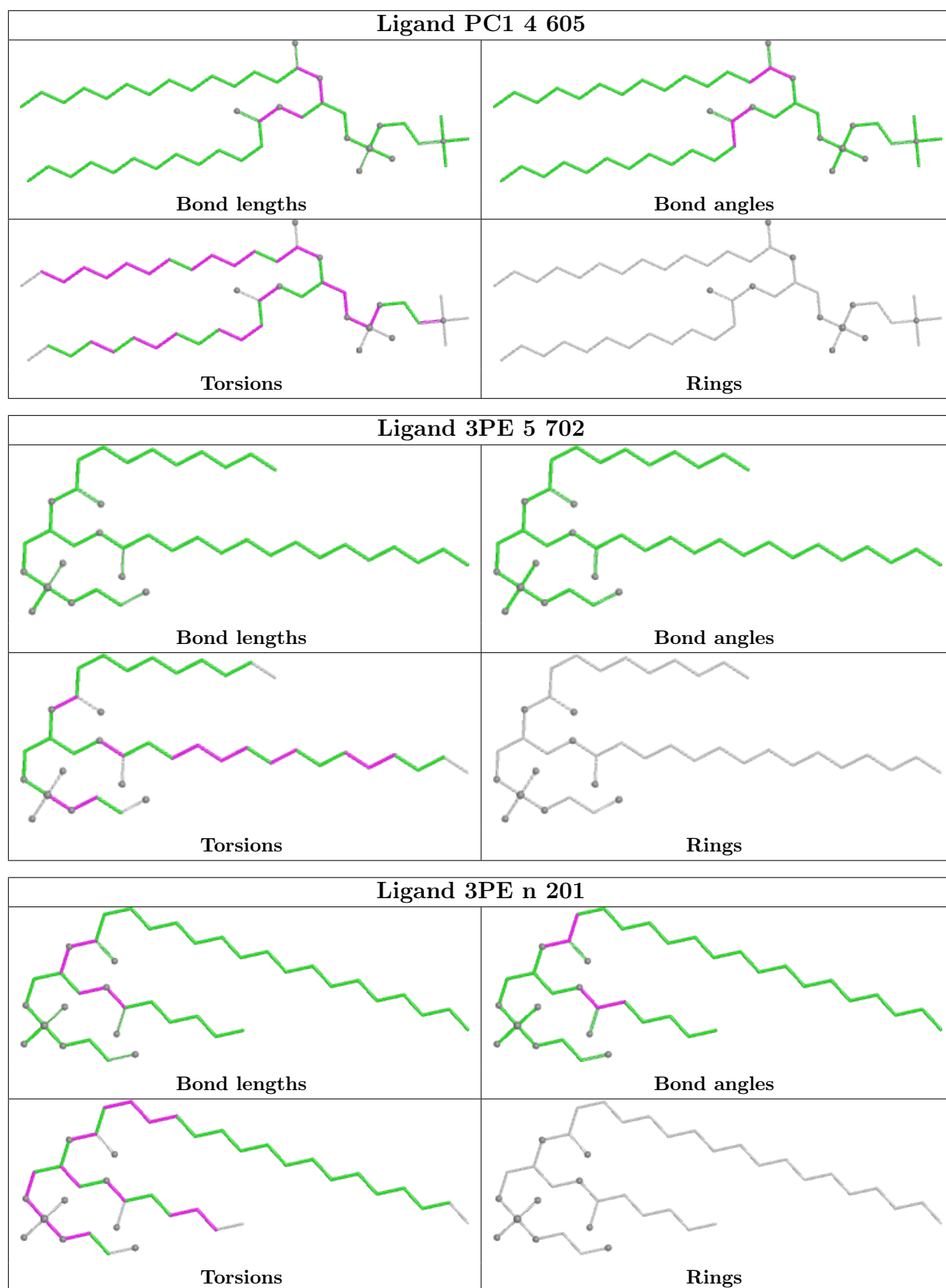
Mol	Chain	Res	Type	Atoms
27	1	402	3PE	C11-O13-P-O14
27	4	603	3PE	C1-O11-P-O12
27	4	603	3PE	C1-O11-P-O14
27	4	603	3PE	C11-O13-P-O12
27	4	603	3PE	C11-O13-P-O14

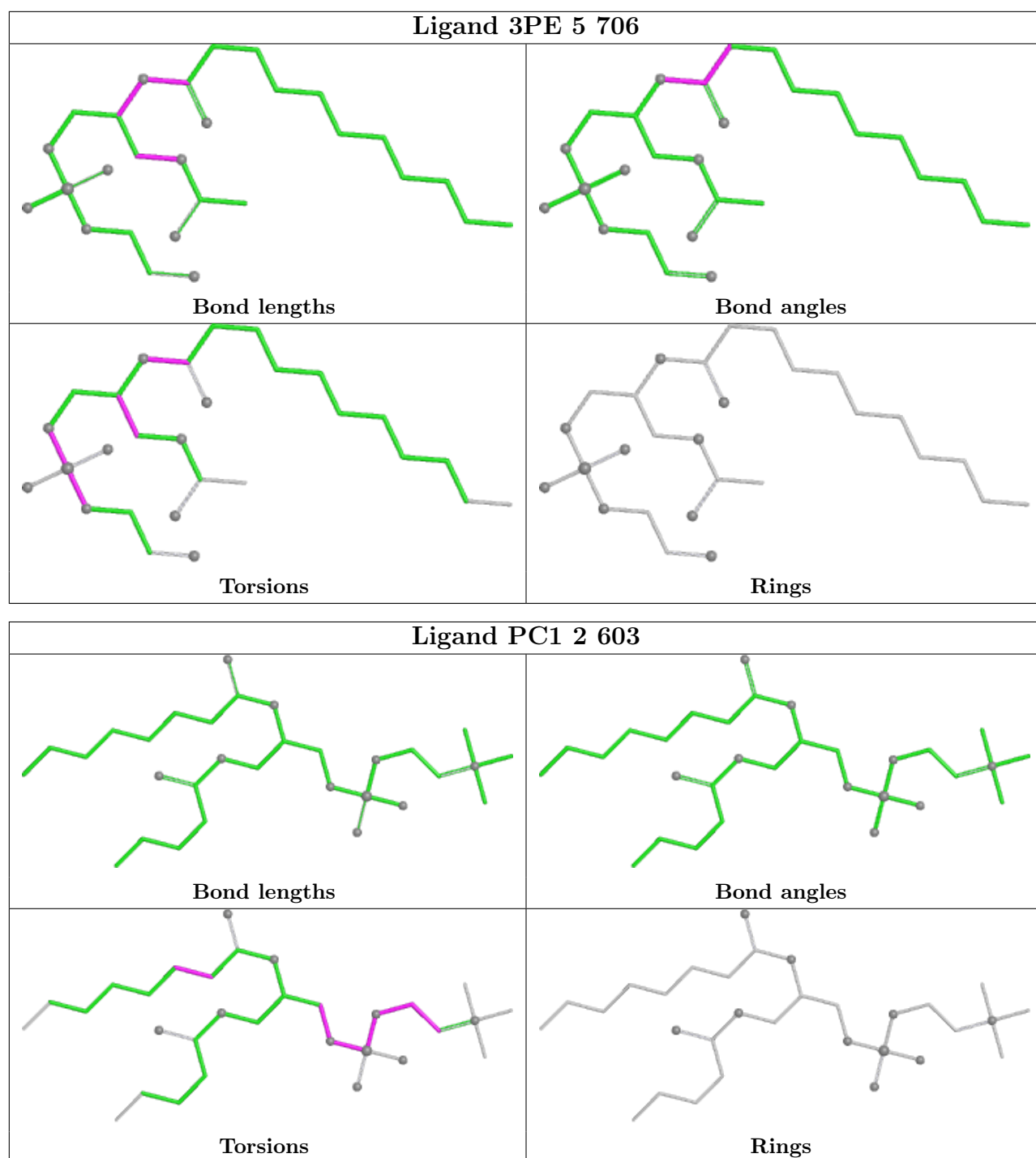
There are no ring outliers.

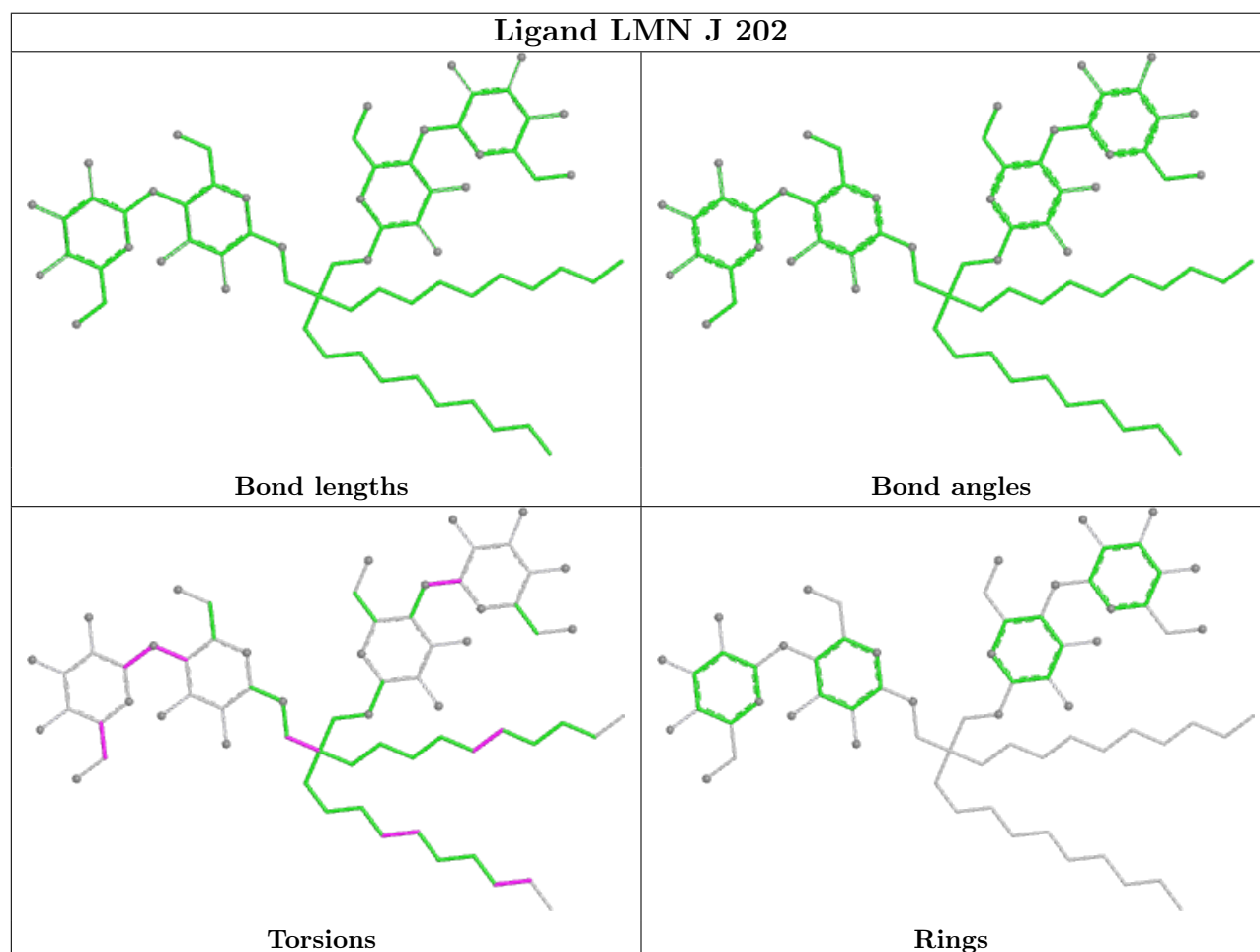
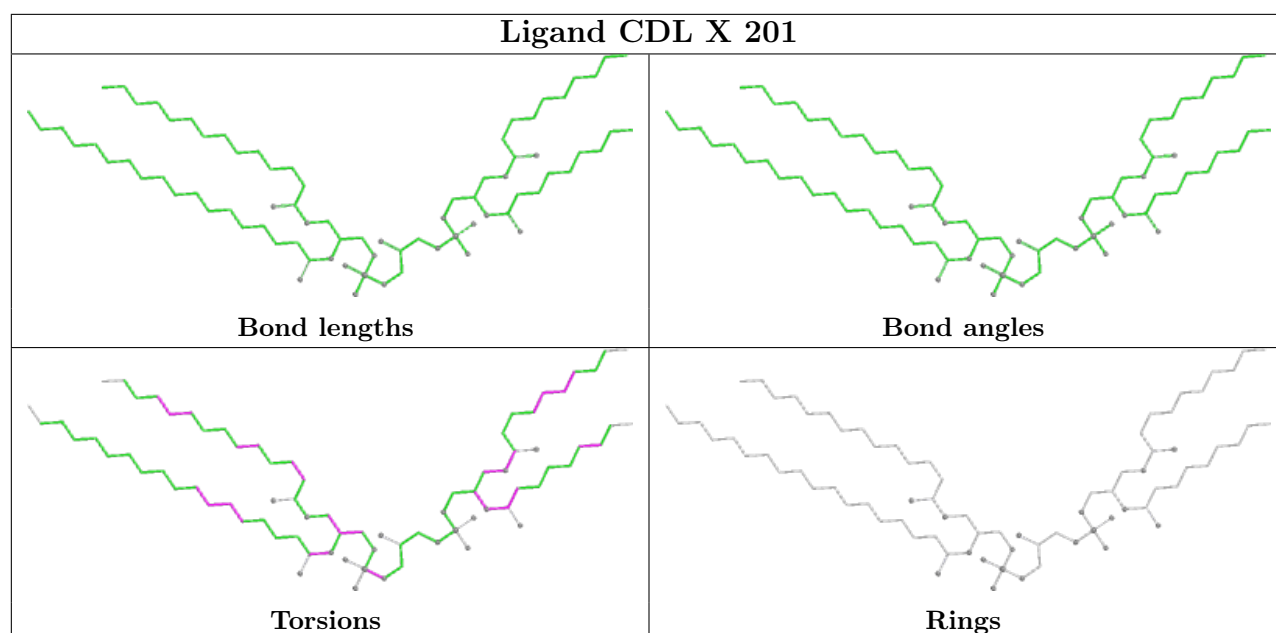
No monomer is involved in short contacts.

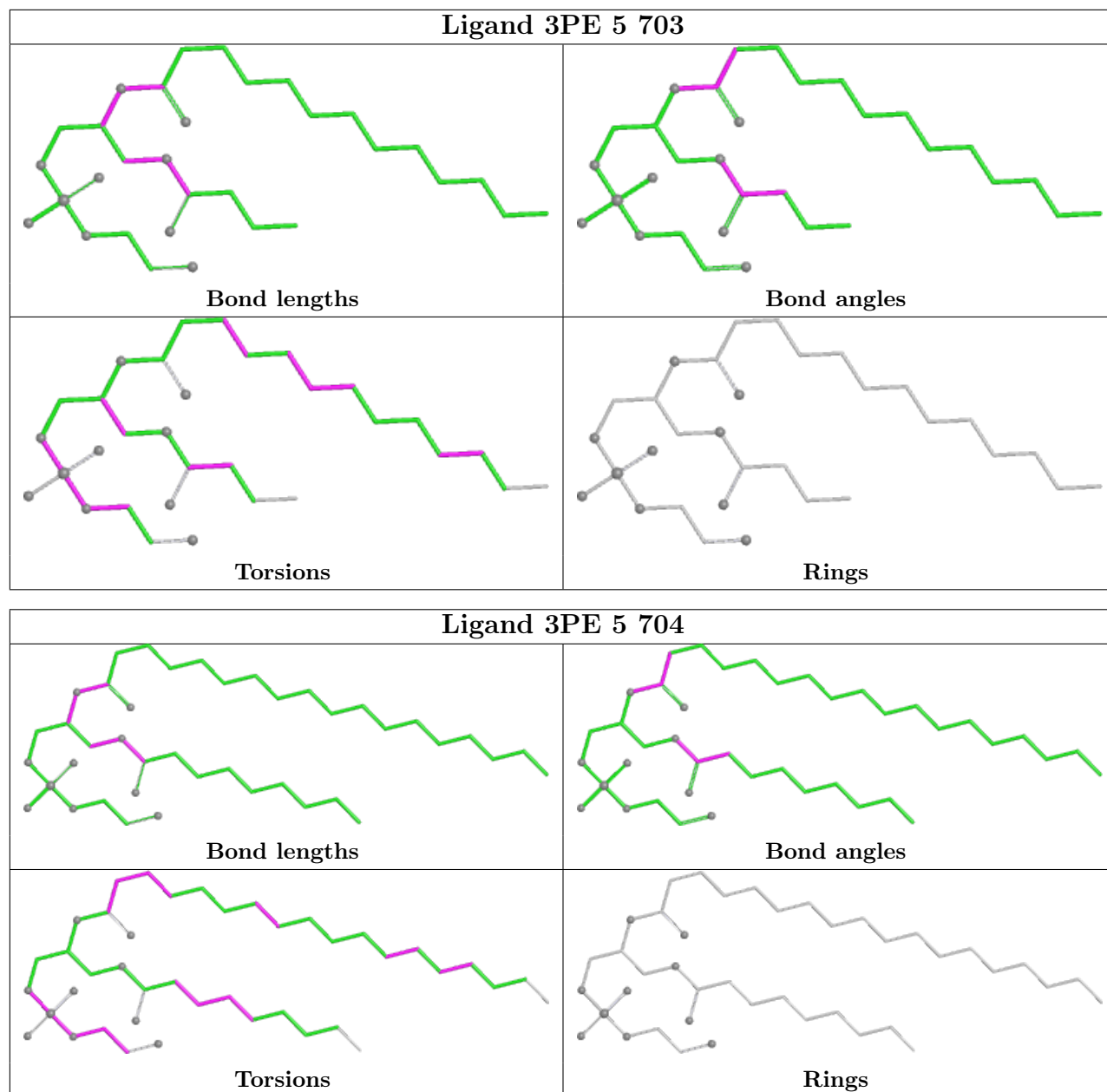
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

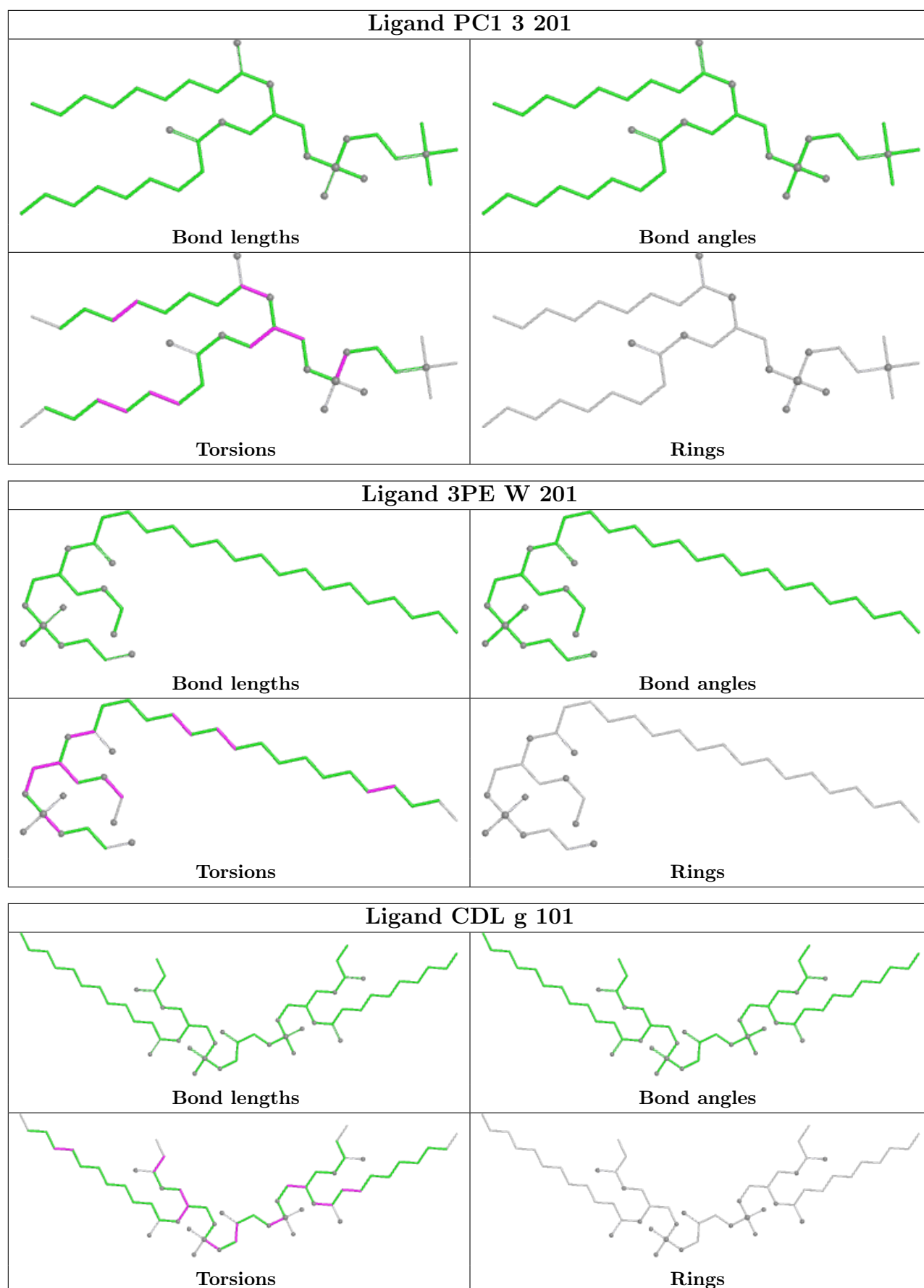


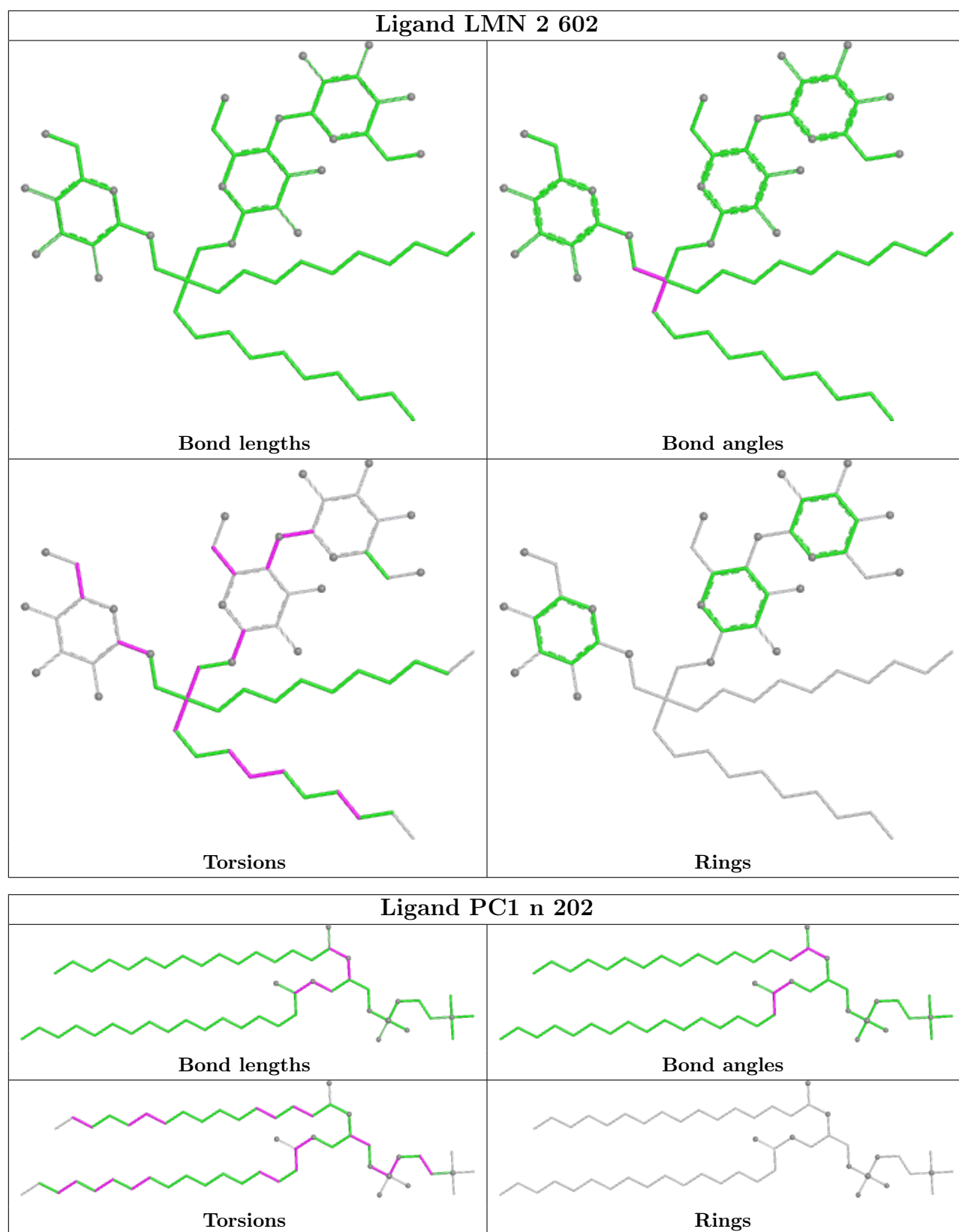


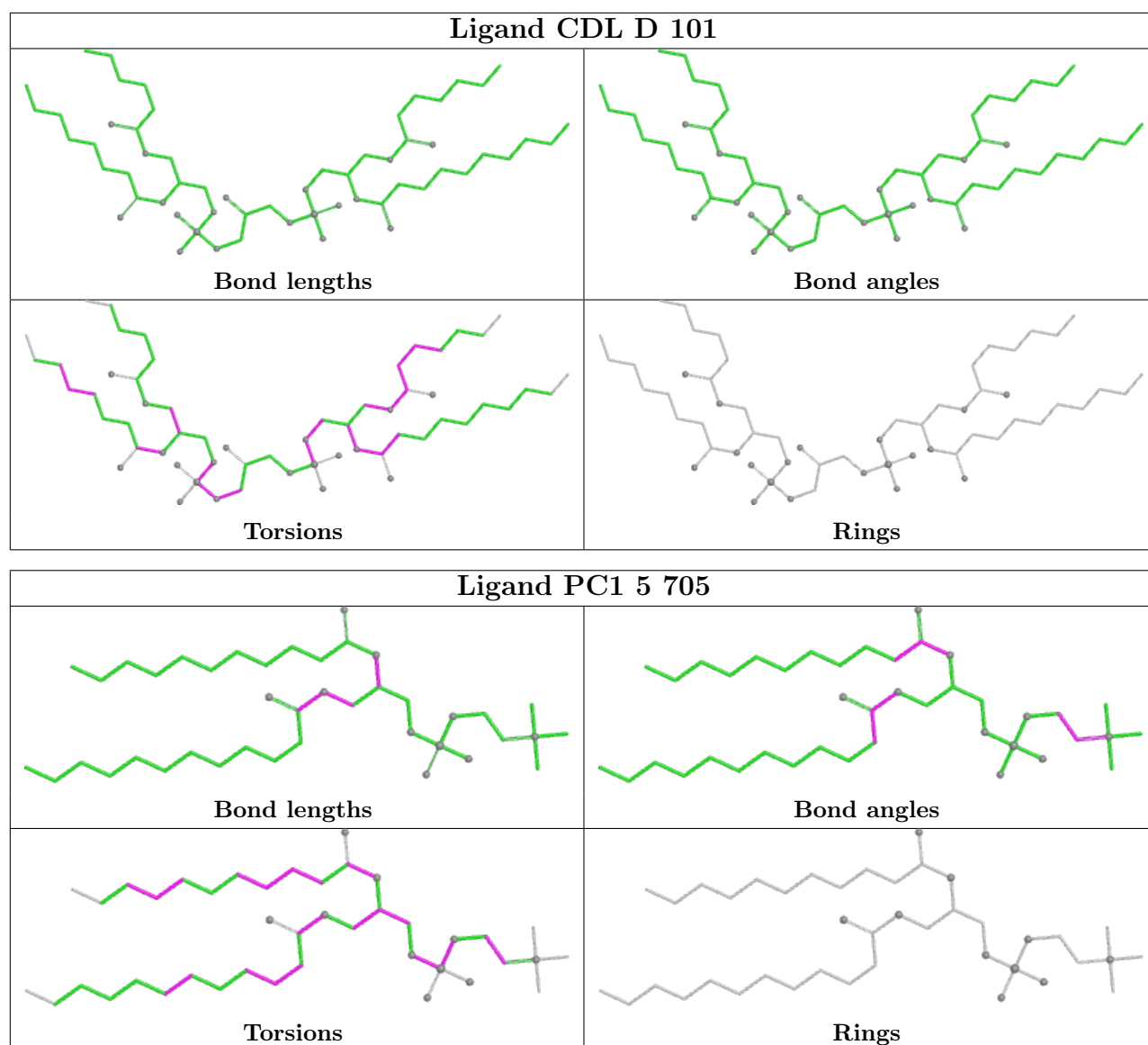


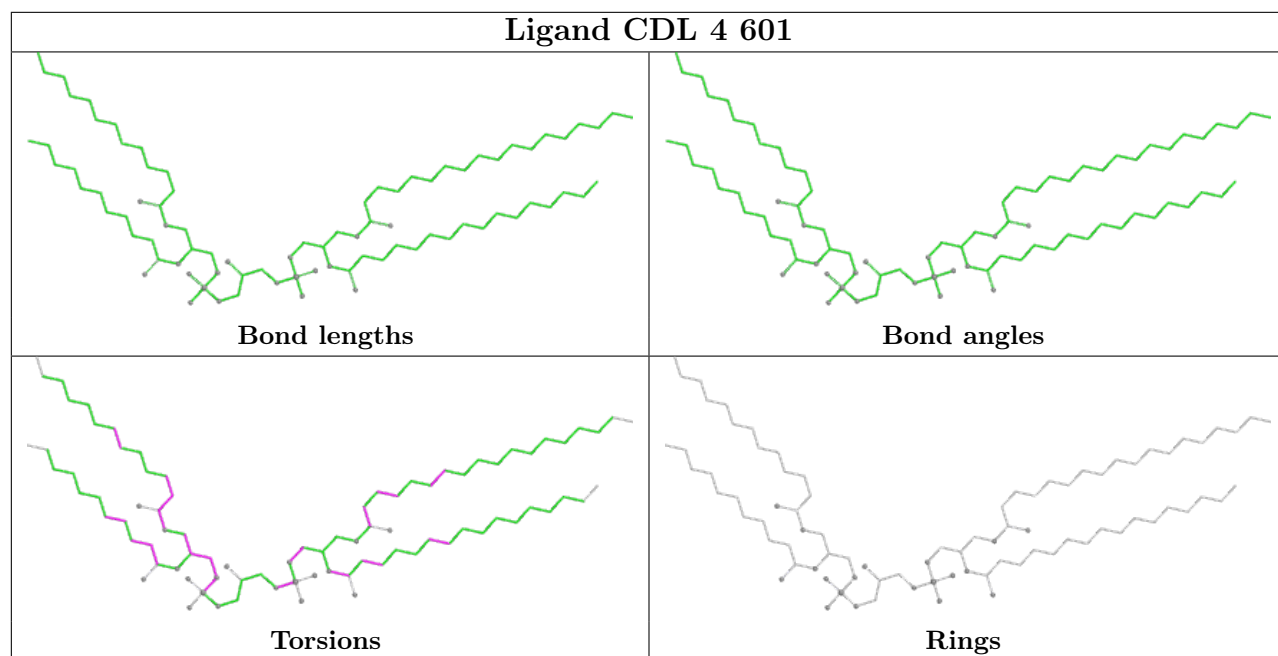
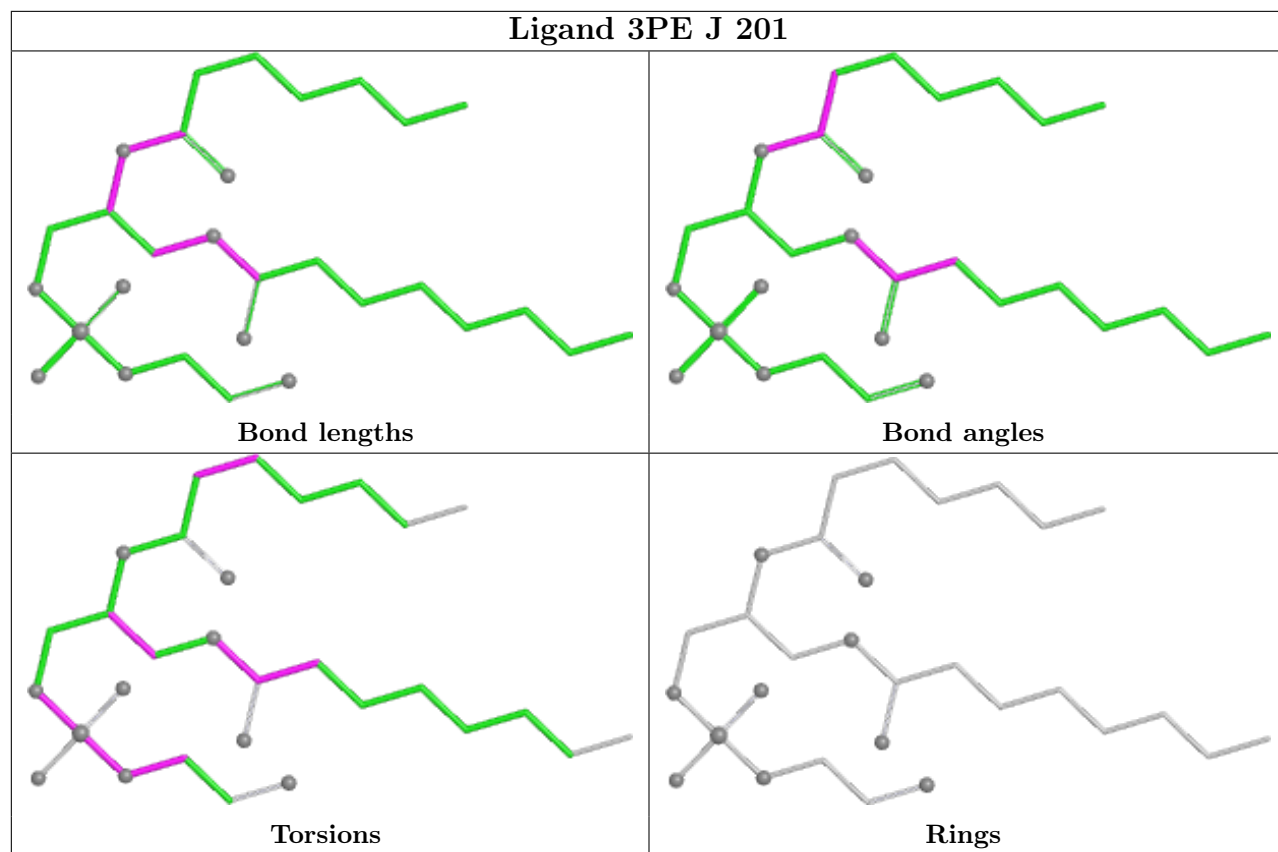


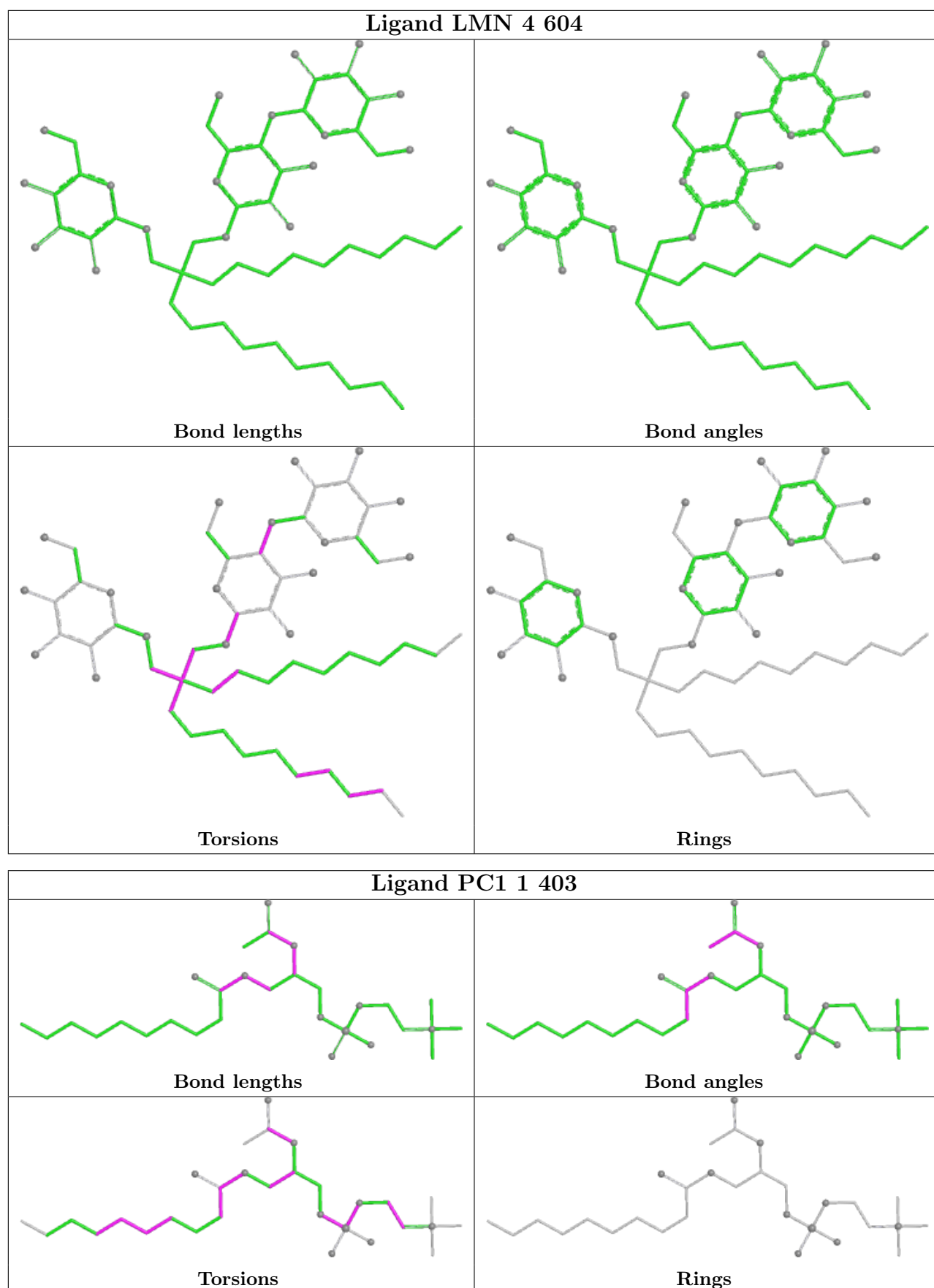


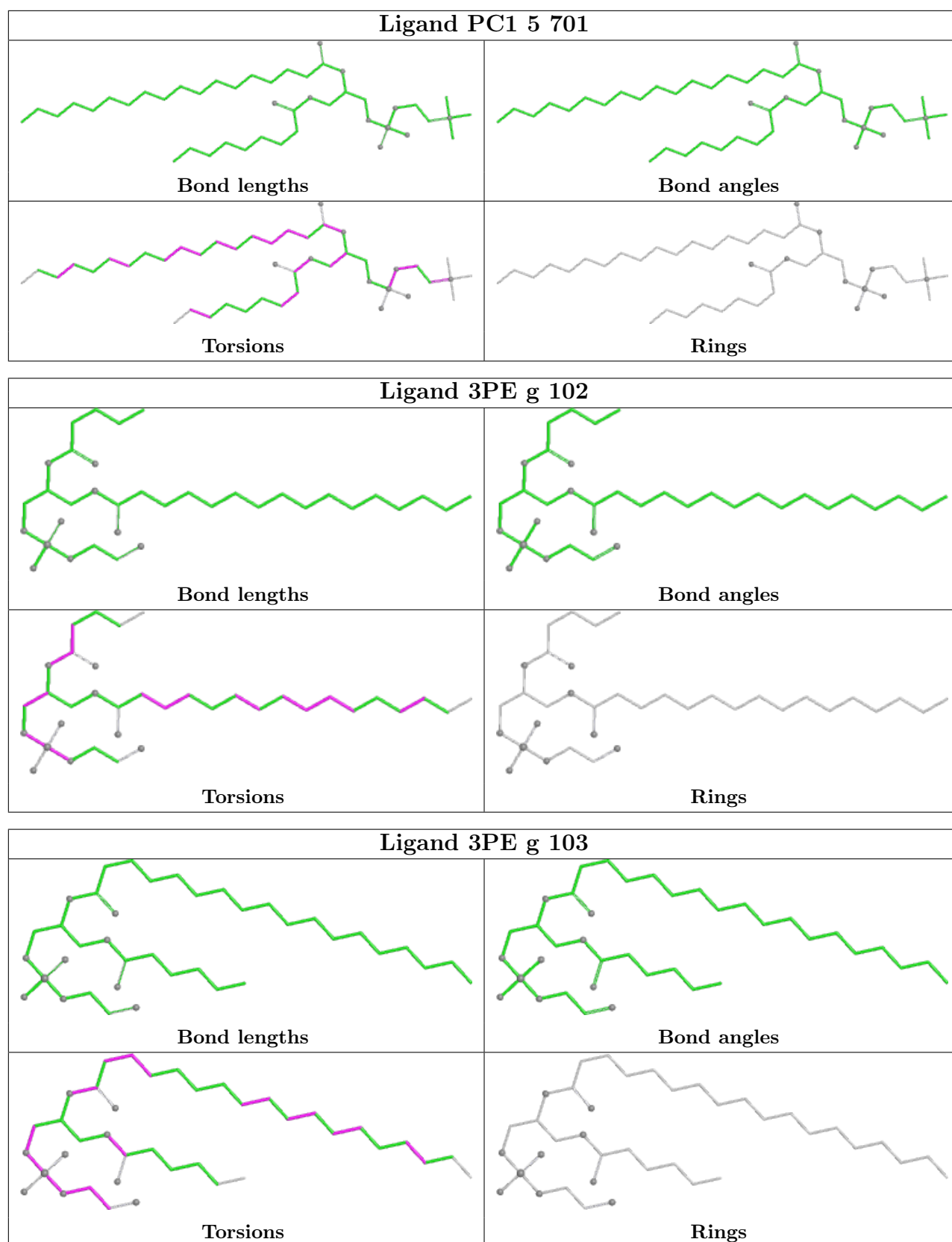


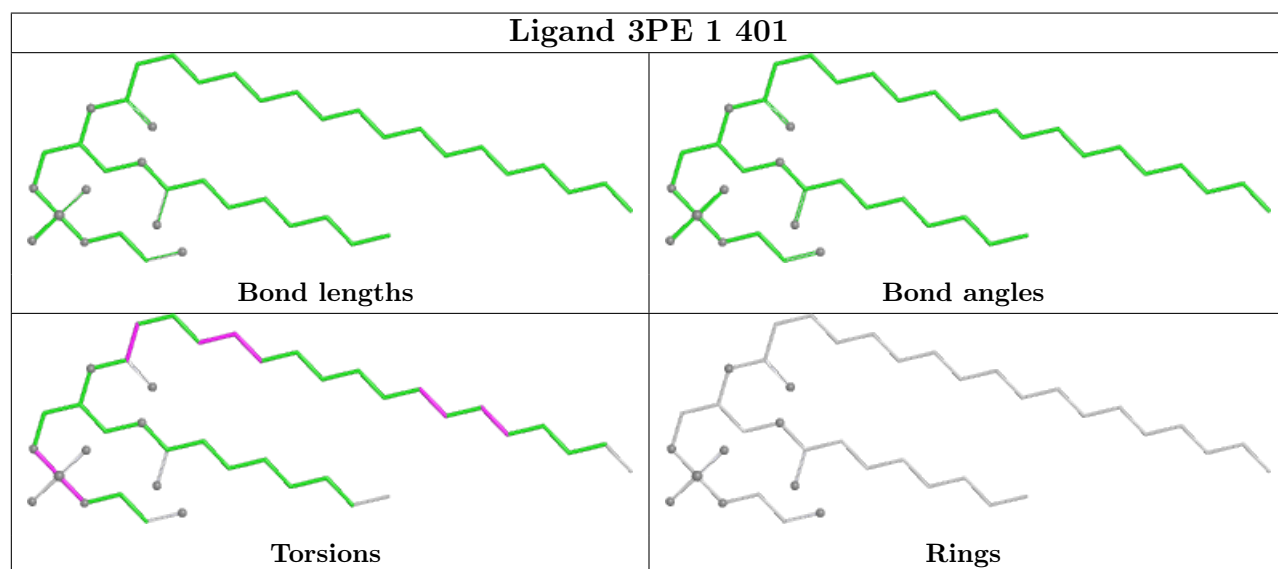
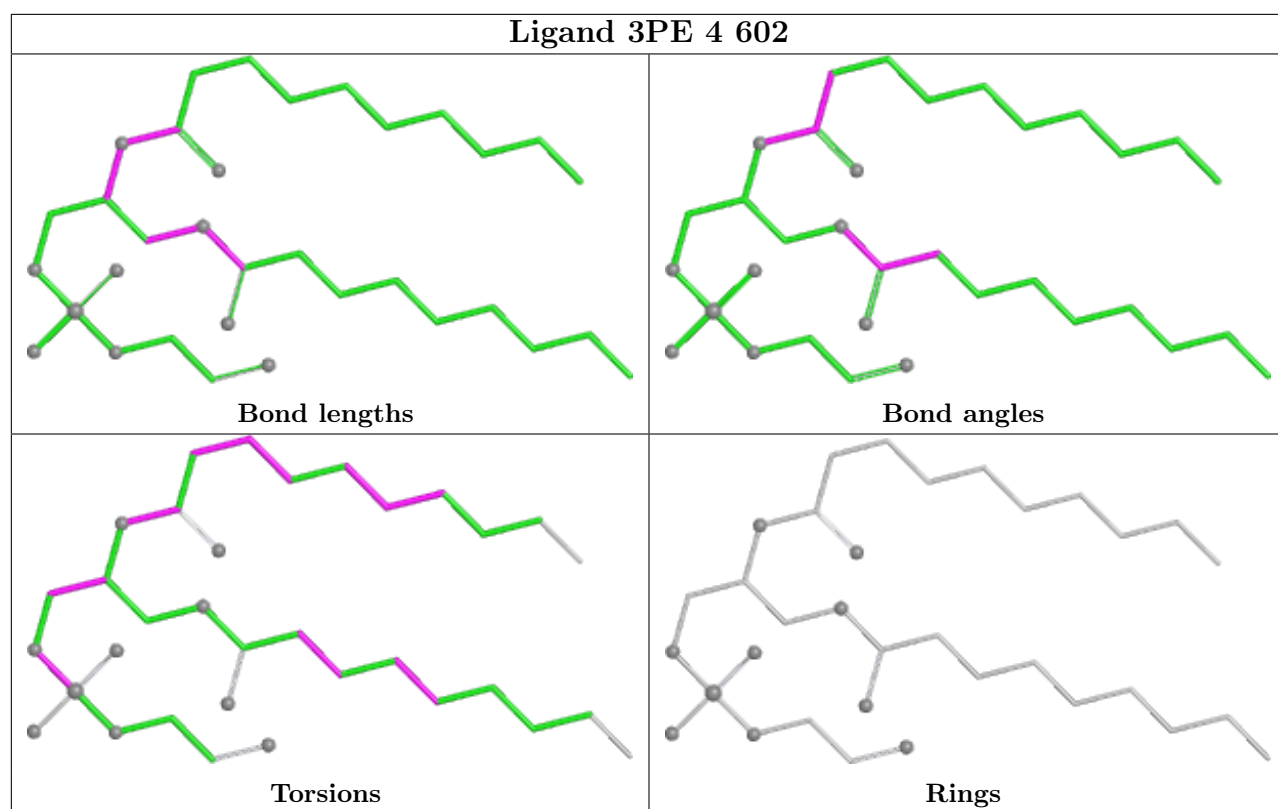


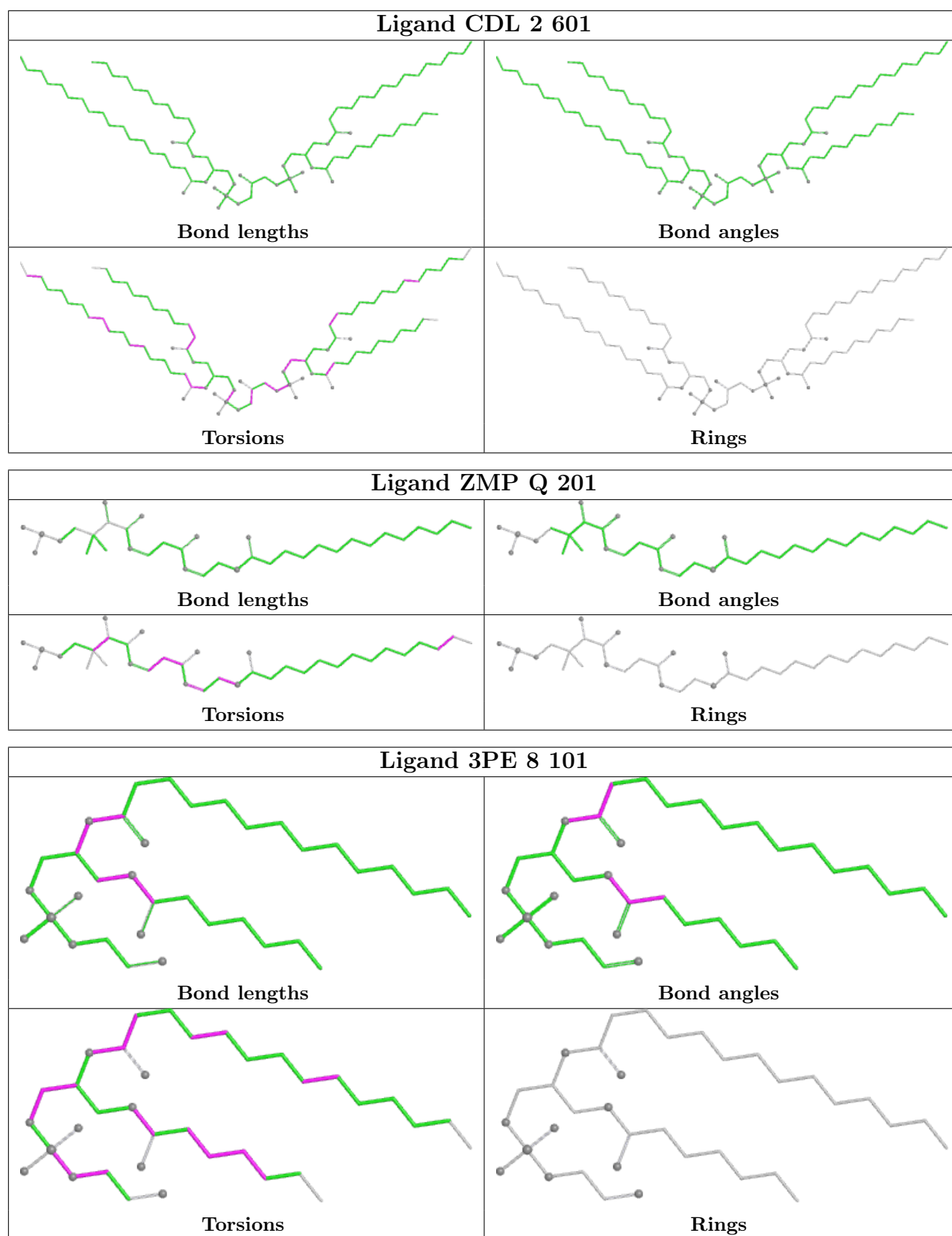


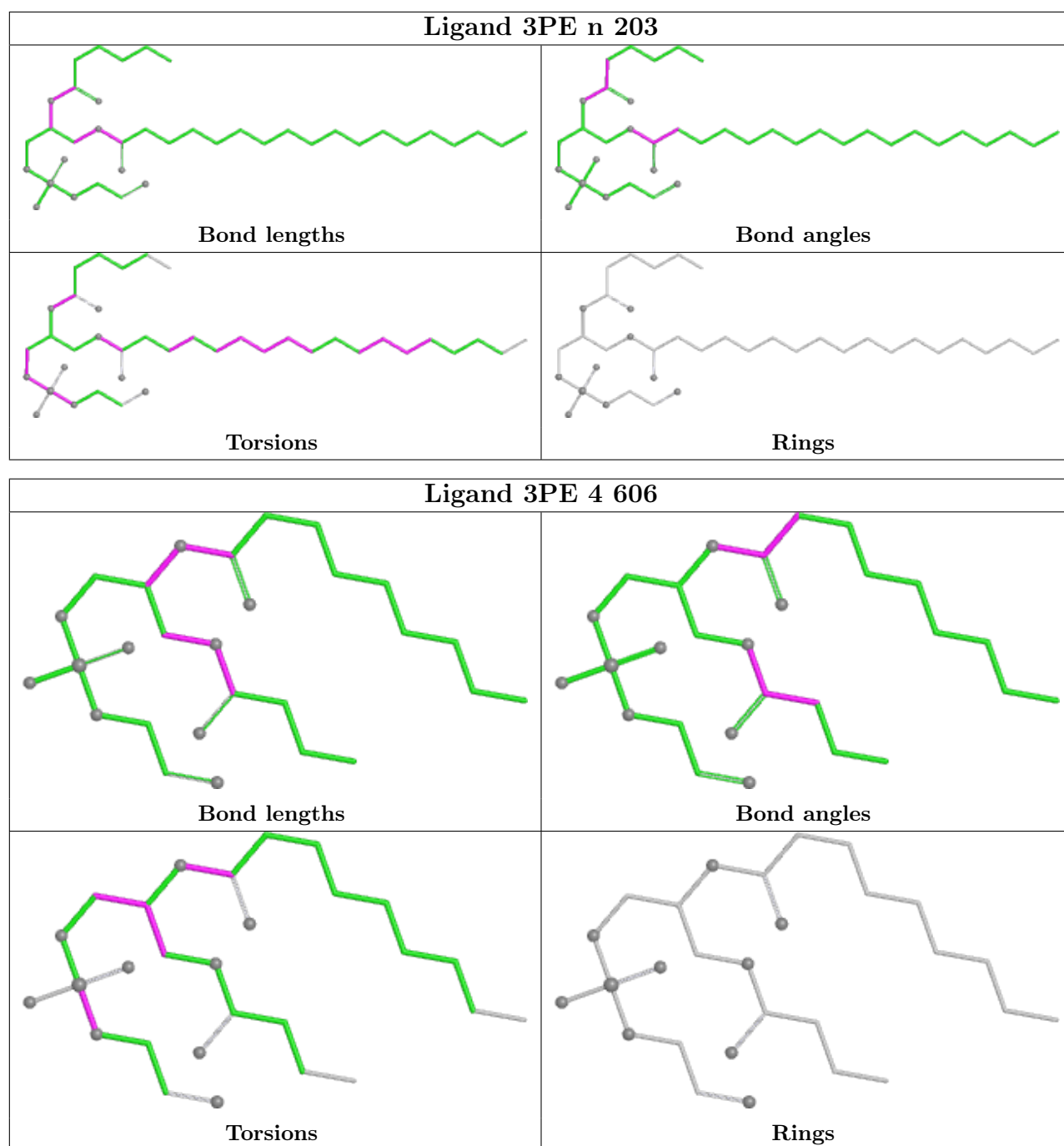












5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

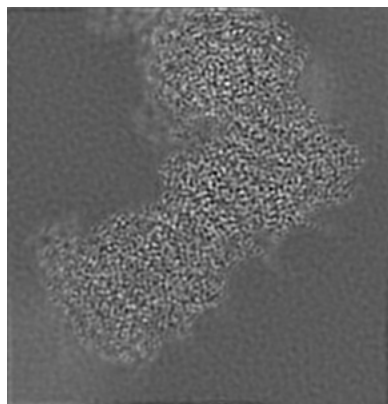
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14796. These allow visual inspection of the internal detail of the map and identification of artifacts.

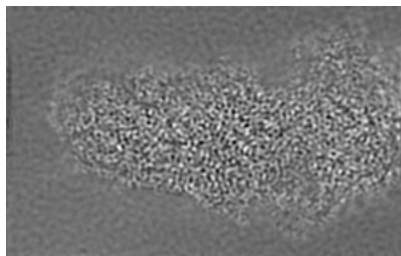
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

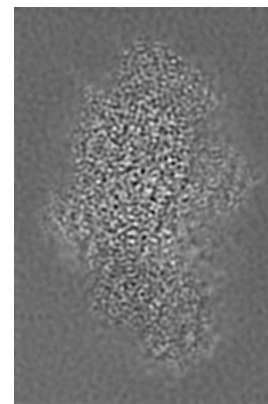
6.1.1 Primary map



X

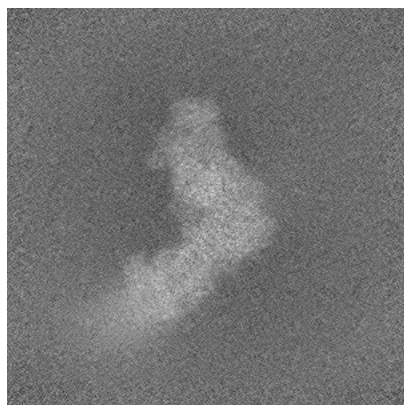


Y

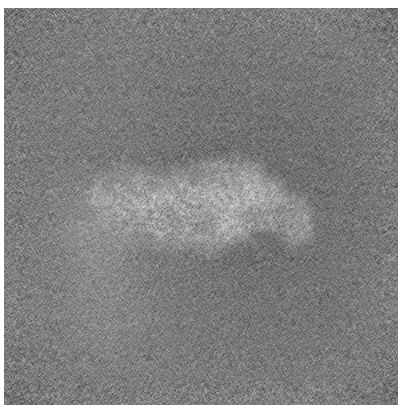


Z

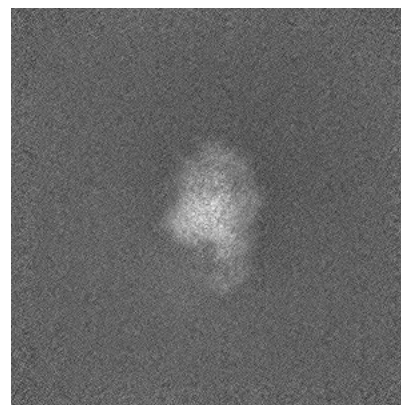
6.1.2 Raw map



X



Y

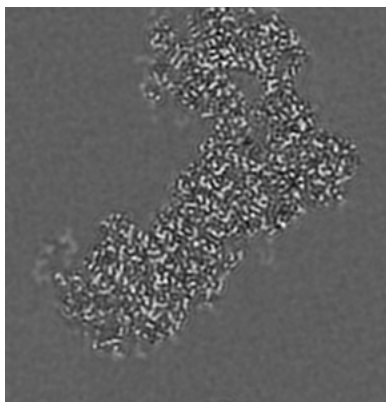


Z

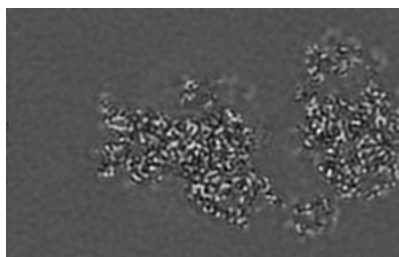
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

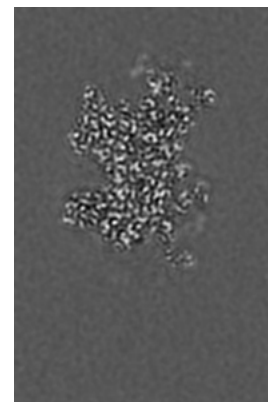
6.2.1 Primary map



X Index: 86

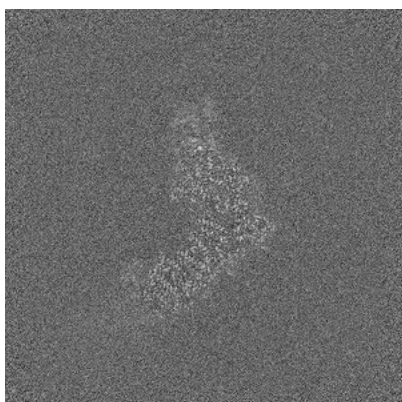


Y Index: 130

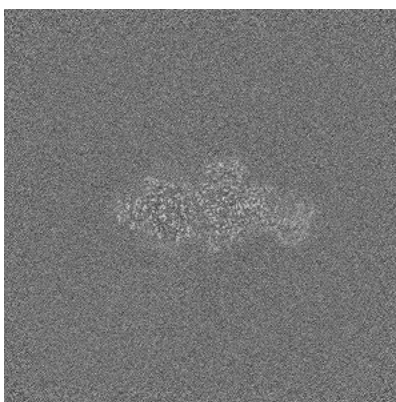


Z Index: 136

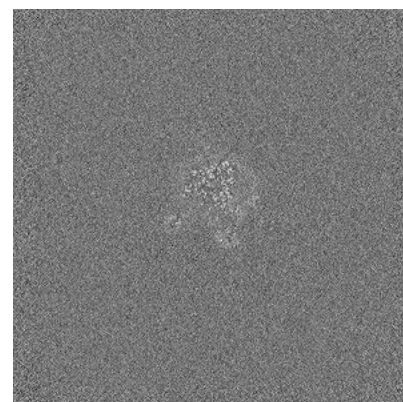
6.2.2 Raw map



X Index: 294



Y Index: 294

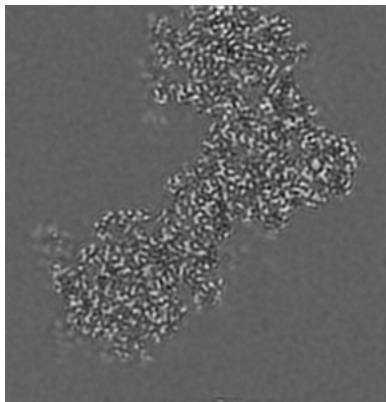


Z Index: 294

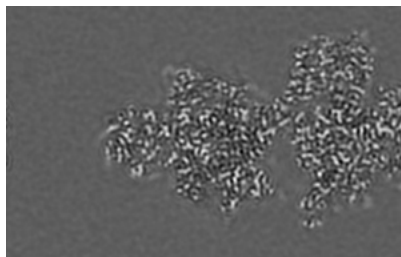
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

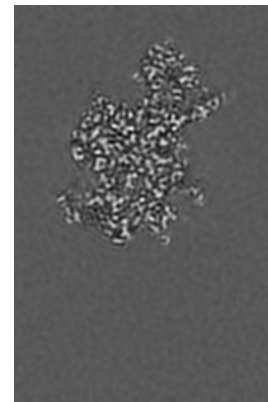
6.3.1 Primary map



X Index: 92

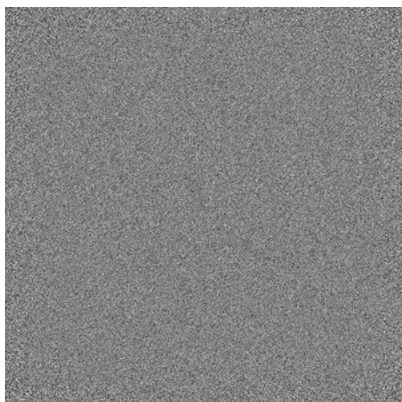


Y Index: 140

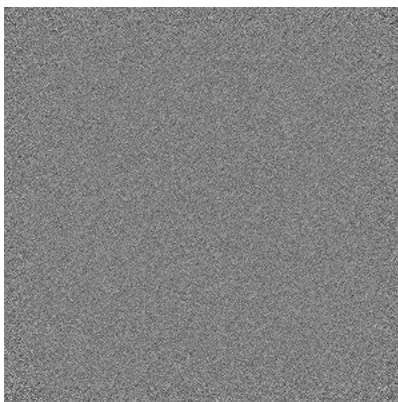


Z Index: 145

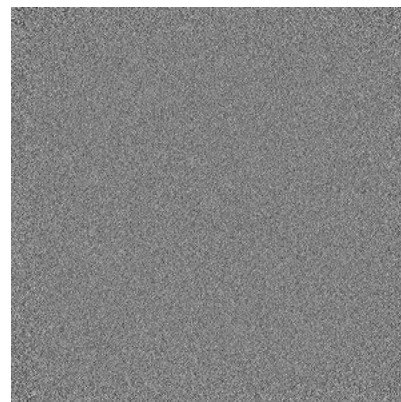
6.3.2 Raw map



X Index: 0



Y Index: 0

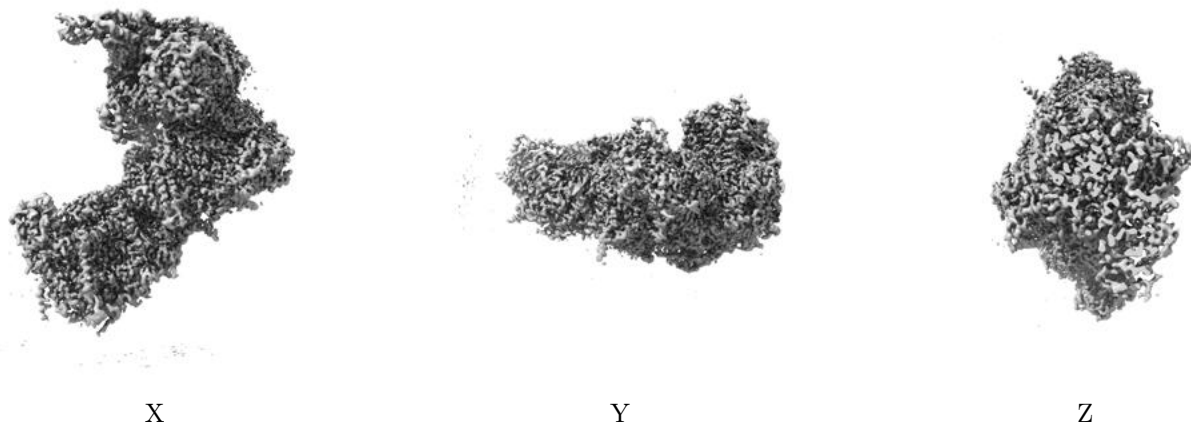


Z Index: 0

The images above show the largest variance slices of the map in three orthogonal directions.

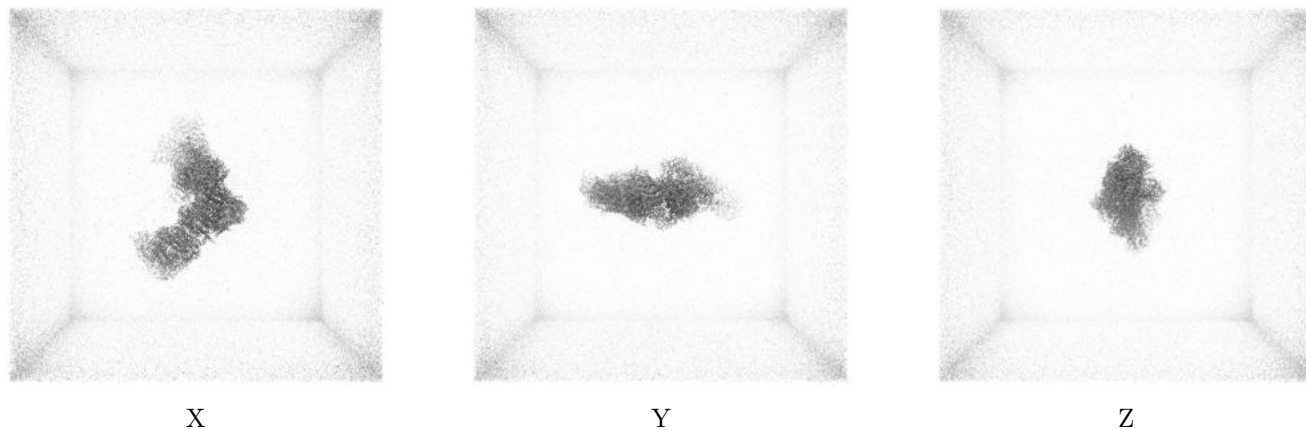
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

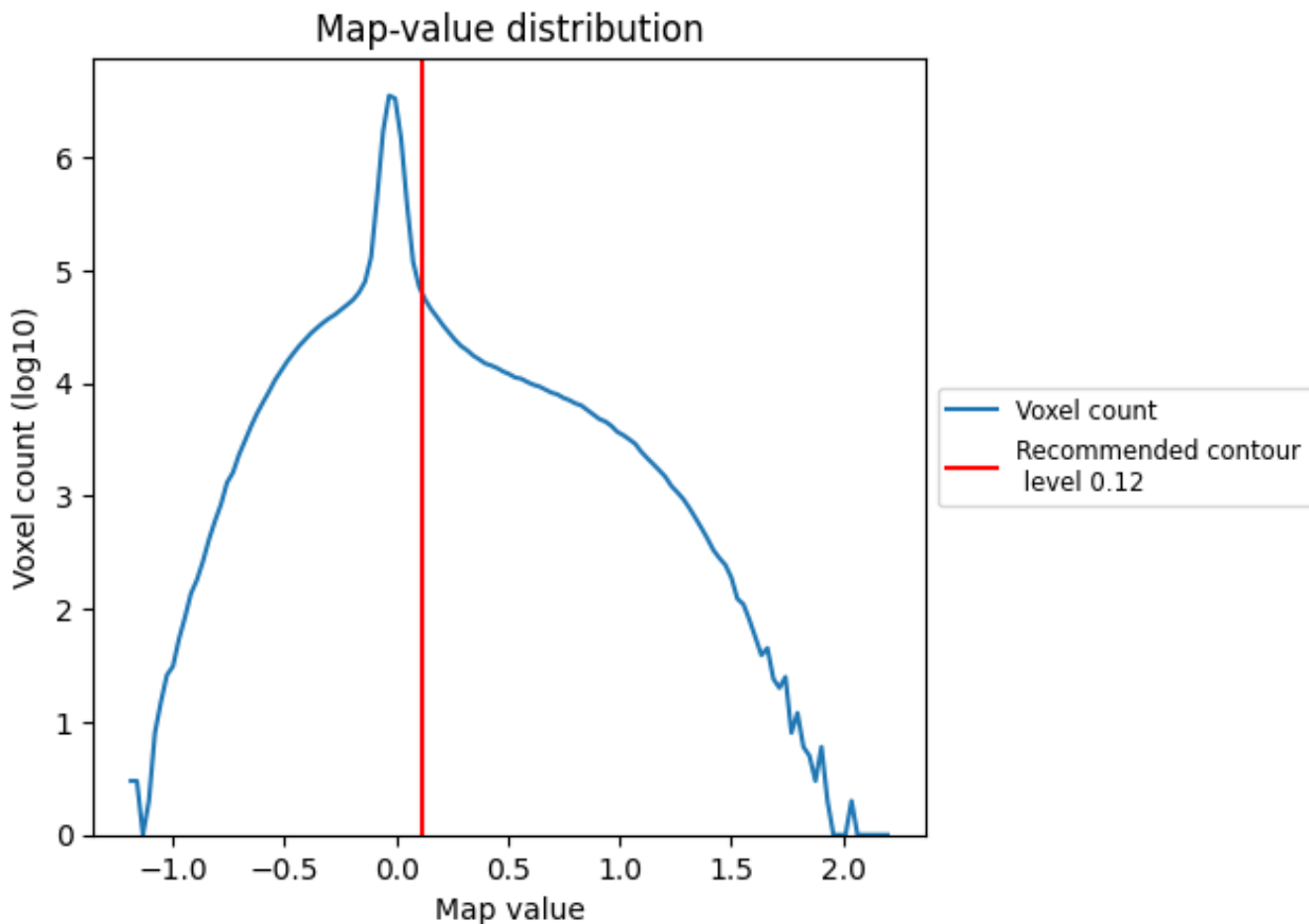
6.5 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

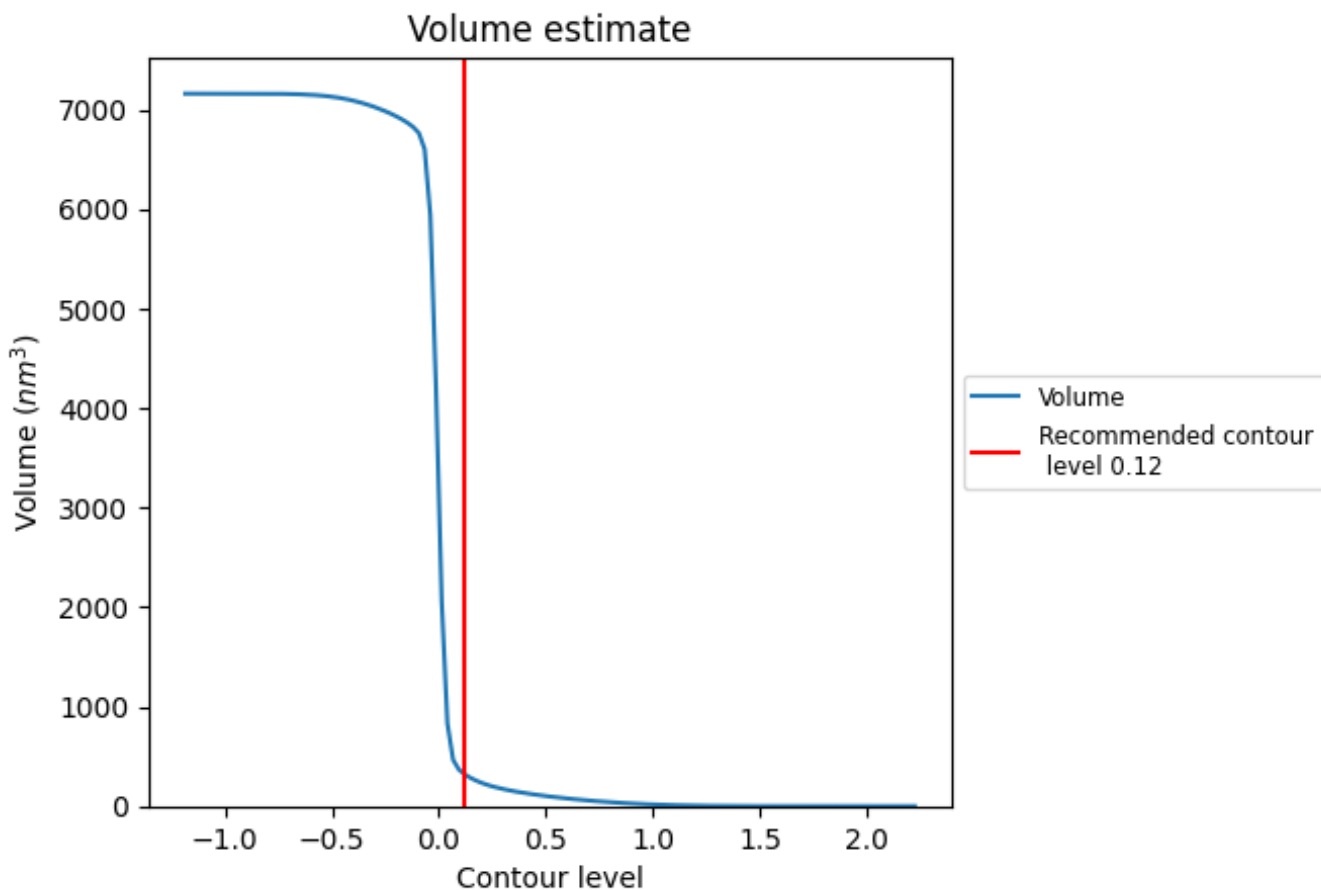
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 320 nm³; this corresponds to an approximate mass of 289 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

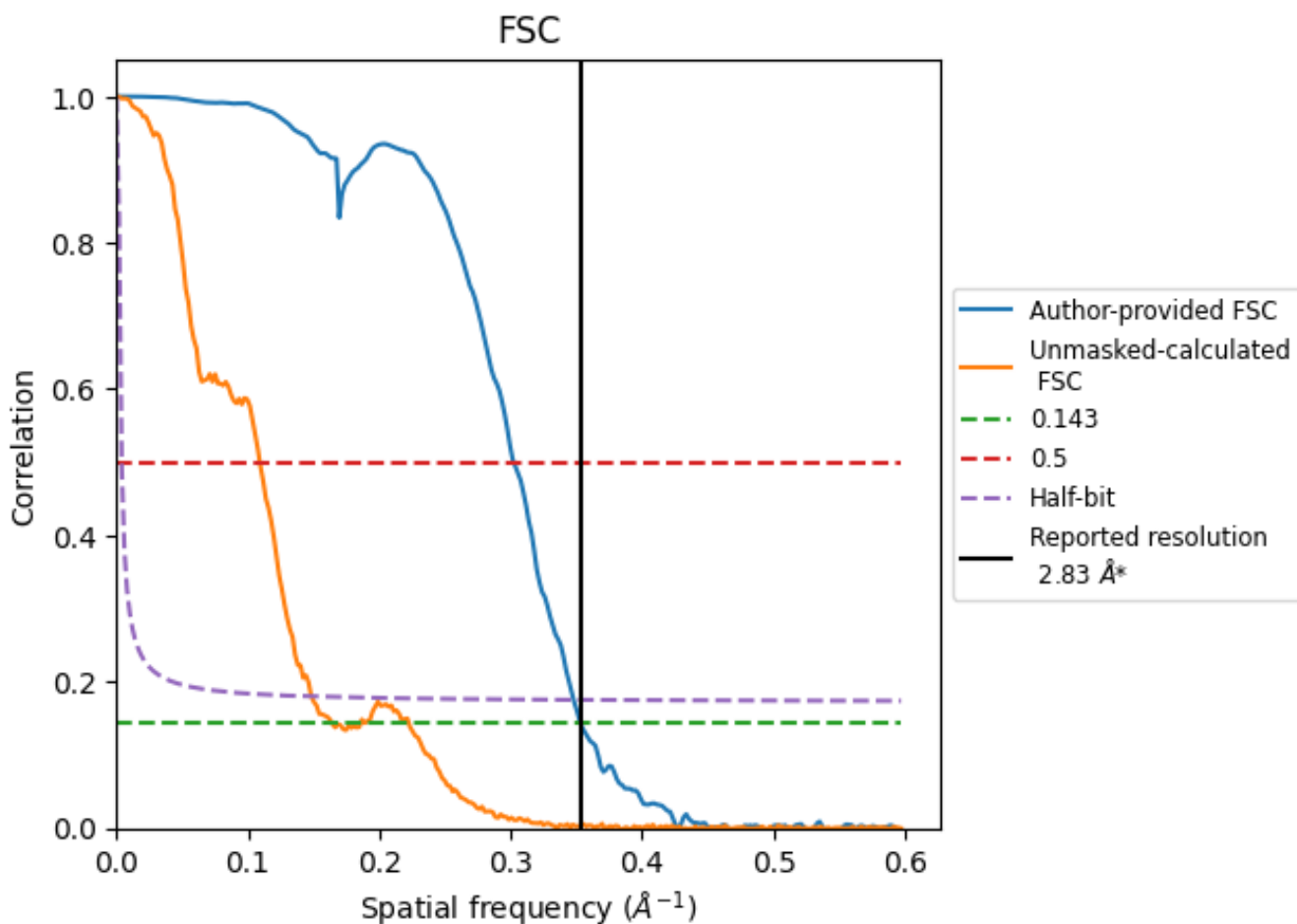
7.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.353 Å⁻¹

8.2 Resolution estimates [i](#)

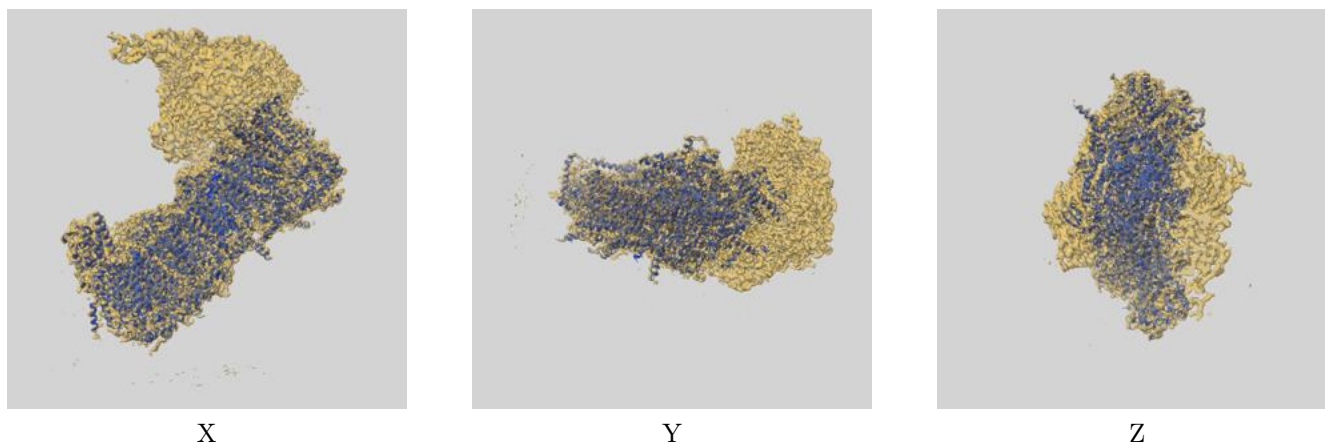
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.83	-	-
Author-provided FSC curve	2.83	3.31	2.87
Unmasked-calculated*	6.09	9.16	6.74

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.09 differs from the reported value 2.83 by more than 10 %

9 Map-model fit [i](#)

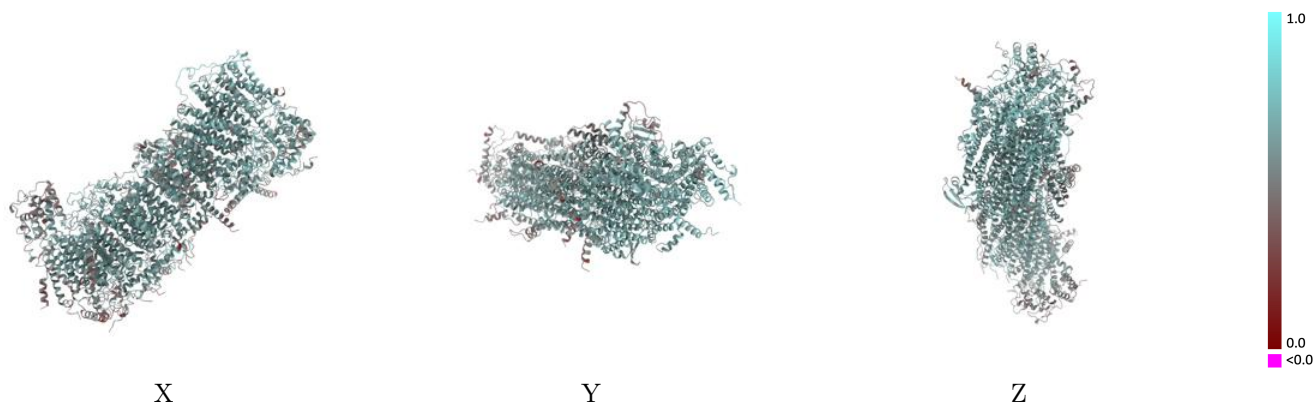
This section contains information regarding the fit between EMDB map EMD-14796 and PDB model 7ZME. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



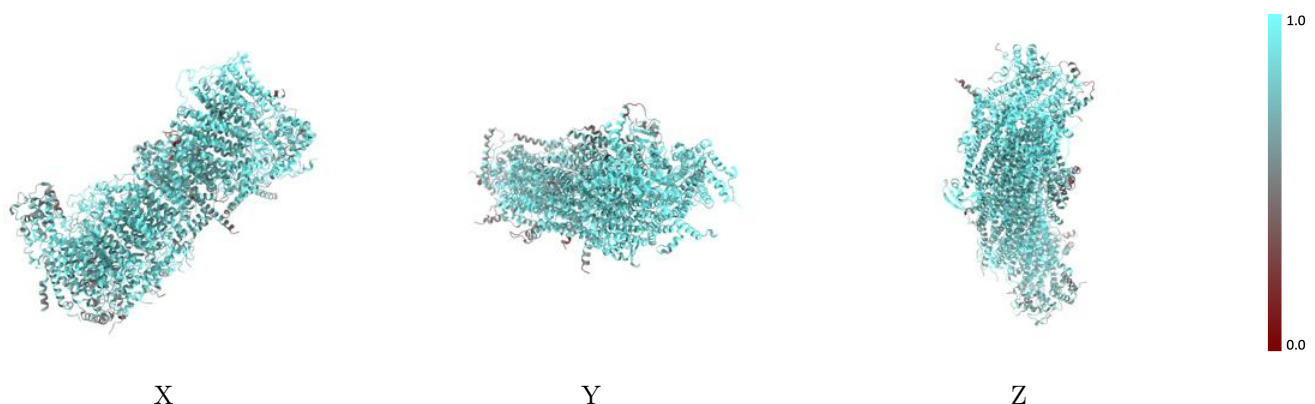
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [\(i\)](#)



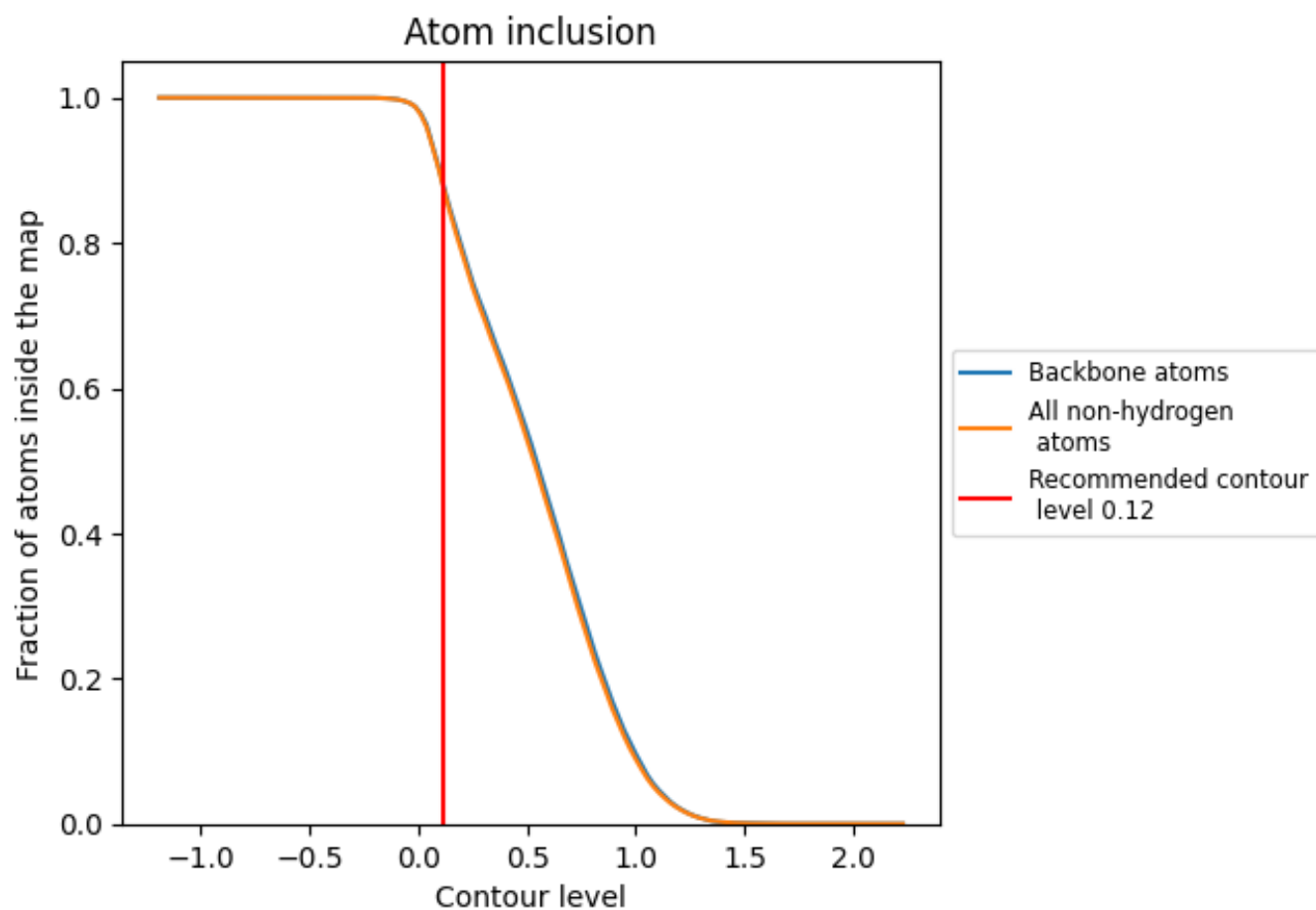
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [\(i\)](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.12).























































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8726	 0.5960
1	 0.9563	 0.6450
2	 0.9400	 0.6410
3	 0.9261	 0.6270
4	 0.9264	 0.6290
5	 0.9002	 0.6030
6	 0.8994	 0.6080
8	 0.6256	 0.4540
9	 0.8035	 0.5620
D	 0.9374	 0.6340
J	 0.6965	 0.5030
L	 0.9335	 0.6310
Q	 0.6465	 0.4580
R	 0.7839	 0.5400
S	 0.8514	 0.5740
U	 0.9220	 0.6120
W	 0.9005	 0.6230
X	 0.9160	 0.6160
a	 0.8090	 0.5430
b	 0.8452	 0.5780
c	 0.7230	 0.4780
d	 0.8654	 0.5840
e	 0.7400	 0.5080
g	 0.9015	 0.5920
i	 0.7918	 0.5460
j	 0.8998	 0.5970
n	 0.7104	 0.5340

